

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number:113398

TO: Michael Borin

Location: rem/2a55/2c70

Art Unit: 1631

Wednesday, February 04, 2004

Case Serial Number: 09/582486

From: Toby Port

Location: Biotech-Chem Library

Remsen 1A59

Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Borin,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port



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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

OM protein - protein search, using sw model

February Run on:

3, 2004, 17:33:58; Search time 21 Seconds (without alignments) 1424.212 Million cell updates/sec

US-09-582-486-1 1637 1 MDTTVPTFSLAELQQGLHQD......ATFQDWIGGNYVNIRRTSKA 311

Perfect score: sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 (otal number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

searched:

finimum DB seq length: 0 faximum DB seq length: 2000000000

maries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 B PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:* pir4:* atabase

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	deacetoxycephalosp	deacetoxycephalosp	deacetoxycephalosp	deacetoxycephalogo	deacetoxycephalosp	deacetoxycephalosn	deacetoxycephalosp	deacetoxycephalosp	isopenicillin N sv	z	2	Sopenicillin N	: 5		isopenicillin N sv	robable dioxyge	flavonol synthage	isopenicillin N av	isopenicillin N sv	gibberellin 20-oxi	flavonol synthage	isopenicillin N sv	i ron/as	isopenicillin N sv	100 ut	gibberellin 20-oxi	,	iconemicilin N ev	n
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	esult No.		7	m	4	ហ	ø	7	Φ		10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

probable gibberell	leucoanthocvanidin	Jeucoanthorvanidin	gibberellin 20-oxi	naringenin 3-dioxv	SRG1 protein - Ara	1-aminocyclopropan	probable oxidoredu	SRG1 protein-relat	gibberellin 20-oxi	hypothetical prote	leucoanthocyanidin	dioxygenase iron	ethylene-forming e	probable flavonol	gibberellin 20-dio
T09675	T05119	T08008	T10222	S31921	S44261	T47932	C83628	T05551	T06787	T41002	T07972	S47972	T09145	T01606	T06439
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	7.4	7.4	7.2	7.2	7.2	7.2		7.1	7.0	7.0	7.0	6.9	6.9	6.9	6.9

RESULT 1

deacetoxycephalosporin C synthetase [imported] - Streptomyces clavuligerus

Cispecies: Streptomyces clavuligerus
Cispecies: Streptomyces clavuligerus
Cipate: 20-Oct.2000 #sequence_revision 20-Oct.2000 #text_change 24-Aug-2001
Cipate: 20-Oct.2000 #sequence_revision 20-Oct.2000 #text_change 24-Aug-2001
Cipate: 20-Oct.2000 #sequence_revision 20-Oct.2000 #text_change 24-Aug-2001
Cipate: 20-Oct.2001
Cipa

A;Residues: 1-311 <KOV>
A;Cross-references: EMBL:M32324; PIDN:AAA26715.1 C;Genetics: A;Gene: ceff C;Superfamily: isopenicillin N synthase

Gaps . 0 Length 311; Indels Score 1629; DB 2; Pred. No. 4.9e-140; 0; Mismatches 1; Query Match
Best Local Similarity 99.7%;
Matches 310; Conservative

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9 9 1 MDTTVPTFSLABLQQGLHQDBFRRCLRDKGLFYLTDCGLTDTELKSAKDLVJDFFEHGSE 1 MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE g

61 AEKRAVTSPVPTMRRGFTGLESESTAQITWTGSYSDYSMCYSMGTADNLFPSGDFGRIWT 120 61 AEKRAVISPVPIMRRGFIGLESESTAQIINIGSYSDYSMCYSMGTADNLFPSGDFERIWT 120 g ઠે

QYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRM 180 121 ò g

240 240 APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA 181 g ò

300 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300 241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 241 셤 ò

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RESULT 2

A32043
deacetoxycephalosporin C synthetase - Streptomyces clavuligerus C;Species: Streptomyces clavuligerus

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C;Species: Streptomyces clavuligerus
C;Species: Streptomyces clavuligerus
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 19-May-2000
C;Accession: A39204; A23713
R;Kovacevic, S.; Miller, J.R.
B;Kovacevic, S.; Miller, J.R.
J; Bacteriol. 173, 398-400, 1991
A;Title: Cloning and sequencing of the beta-lactam hydroxylase gene (ceff) from Streptom
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C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 19-May-2000
C;Accession: 840253
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                       A, Residues: 1-310 <COQ>
A, Residues: 1-310 <COQ>
A, Cross-references: EMBL: Z21687; NID: 9438193; PIDN: CAA79803.1; PID: 9438194
A, Note: the source is designated as Nocardia lactamdurans
A, Note: the source is designated.
OYFDROYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRM
                                                                                       181 APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
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S9.0%; Score 965.5; DB 2
Best Local Similarity 61.2%; Pred. No. 7.8e-80;
Matches 186; Conservative 37; Mismatches 80
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| NYINIRKTAAA 313
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A, Recession: S40253
A, Stacuss: preliminary
A, Molecule type: DNA
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                     C; Date: 13-Jul-1989 #sequence_revision 13-Jul-1989 #text_change 19-May-2000
C; Accession: A32043
R; Kovacevic, S.; Waigel, B.J.; Tobin, M.B.; Ingolia, T.D.; Miller, J.R.
J; Bacceriol. 171, 754-760, 1989
A; Title: Cloning, characterization, and expression in Escherichia coli of the Streptomychacesion: A32043; MUID:89123150; PMID:2644235
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-311 < KOV>
C; Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
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C, Species: Streptomyces lactamdurans
C, Species: Streptomyces lactamdurans
C, Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-2000
C; Accession: S10900; S28183
R; Coqque, J.J.R.; Marthn, J.F.; Liras, P.
Mol. Gen. Genet. 236, 453-458, 1993
A; Title: Characterization and expression in Streptomyces lividans of cefD and cell avalugetus.
A; Reference number: S10900; MUID:93173127; PMID:8437592
A; Accession: S10900
A; Molecule type: DNA
A; Residues: 1-314 <CCO>
A; Cooss-references: EMBL:Z13974; NID:949299; PIDN:CAA78376.1; PID:949300
A; Cross-references: RMBL:Z13974; NID:949299; PIDN:CAA78376.1; PID:949300
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241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
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              13-Jul-1989 #sequence_revision 13-Jul-1989 #text_change 19-May-2000
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Pred. No. 7e-100;
41; Mismatches 52; Indels
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Pred. No. 7.5e-140;
1; Mismatches 1;
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Best Local Similarity 69.8%;
Matches 217; Conservative 4
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Best Local Similarity 99.4%;
Matches 309; Conservative
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deacetoxycephalosporin C synthetase - fungus (Acremonium sp.)
NyAlternate names: expandase; hydroxylase
NyAlternate names: expandase; hydroxylase
C;Species: Acremonium sp.
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 19-May-2000
C;Accession: A29711; A41864
R;Samson, S.M.; Dotalaf, J.E.; Slisz, M.L.; Becker, G.W.; Van Frank, R.M.; Veal, L.E.; Yt
Bio/Technology 5, 1207-1214, 1987
A;Title: Cloning and expression of the fungal expandase/hydroxylase gene involved in cepl
A;Reference number: A29711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Bacteriol. 174, 3056-3064, 1992
A,Title: The cefG gene of Cephalosporium acremonium is linked to the cefEF gene and encoc
A,Reference number: A41864, MUID:92234966, PMID:1569032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBIP:97574); this ORF is
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63 QXNALRNLTPRVRRGFSDLEAESTARITKGGEYTDYSMVYSIGLTDNLFPSPAFEAIWTG 122
                                                                                                                                                                                                                                                 RHHVAAPRRDQIAGSSRISSVFFLRPNADFIFSVPLARECGFDVSLDGETATFQDWIGGN 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDITVPIFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.6%; Score 926.5; DB 2; Length 56.7%; Pred. No. 2.9e-76; tive 43; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: DNA
A,Residues: 1-332 <SAM>
A,Rote: the source is designated as Cephalosporium acremonium
A,Note: the source is designated by Fernandez, F.J.; Martin, J.F.
J. Bacteriol. 174, 3056-3064, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain C10
A;Note: sequence extracted from NCBI backbone (NCBIN:104773, P
A;Note: the source is designated as Cephalosporium acremonium
C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
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A;Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-76,'L' <GUT>
                                                                                                                                                                                                                                                                                                                                             302 YVNIR 306
                                                                                                                                                                                                                                                                                                                                                                                         303 YVNLR 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A41864
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                                                                                                                                                 . Biol. Chem. 266, 5087-5093, 1991
Title: Deacetoxycephalosporin C hydroxylase of Streptomyces clavuligerus. Purification;
Reference number: A23713; MUID:91161600; PMID:2002049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NID:g153206; PIDN:AAA26716.1; PID:g153207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 PAPRHHVRSPGAGMREGSDRTSSVFFLRPTTDFSFSVAKARSYGLAVDLDMETAFFGDWI 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 EKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 YFDRQYTASRAVAREVLRATG---TEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leacetoxycephalosporin C synthetase 1 - Lysobacter lactamgenus (strain YK90)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;;Species: Lysobacter lactamgenus
h;Variety: strain YK90
;;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 DITVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Residues: 1-319 «KIM»
A.Cross-references: EMBL:X56660; NID:9769806; PIDN:CAA39984.1; PID:9769808
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DITVPTFSLAELOOGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEA
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 58.6%; Pred. No. 1.8e-77;
Matches 180; Conservative 43; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Experimental source: strain YK90
S, Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
S, Keywords: antibiotic biosynthesis
                                                                                                                                                                                                                                                                                                           ,;Gene: cefF
;;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
                Reference number: A39204; MUID:91100311; PMID:1987130
                                                           Molecule type: DNA
;Residues: 1-318 <KOV>
;Cross-references: GB:M63809; GB:M37186;
;Baker, B.J.; Dotzlaf, J.E.; Yeh, W.K.
Biol. Chem. 266, 5087-5093; 1991
                                                                                                                                                                                                                 ,Accession: A23713
,Molecule type: protein
,Residues: 2-29,92-100 <BAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGNYVNI 305
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Ciders 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 26-May-2000
Ciders 2187-196, 1989
A;Tttle: Cloning and nucleotide sequence determination of the isopenicillin N synthet A;Tttle: Cloning and nucleotide sequence determination of the isopenicillin N synthet A;Reference number: A29894, MUID:88212175; PMID:3130293
A;Residues: 1-329 cLES.
A;Cross-references: GB:M9421; NID:g153328; PIDN:AAA26770.1; PID:g153329
C;Superfamily: isopenicillin N synthase
C;Superfamily: isopenicillin N synthase
C;Keywords: antibiotic biosynthesis; ascorbic acid; iron; metalloprotein; oxidoreduct F;48,212,268/Binding site: iron (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isopenicillin N synthase (EC 1.14.11.-) [similarity] - Streptomyces clavuligerus
                                                                                                                                                                                                                                                                                                                  177 LADTISAVTLIHYPYLEDYPPVKTGPDGTKLSFEDHLDVSMITVLFQTEVQN----LQVE 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 ---FLDCEPLLRFRYFPQVPEHRSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 -SG---DFGRIW------TQYFDRQYTASRAVAREVLRATGTEPDGGVEA--- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 SEABK----RAVTSPVPTMRRGF----TGLESESTAQITWTGSYSDYSMCYSMGT---A 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNLFPSGD----FGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEA-----FLDCE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 PLLRFRYFPQVPEHRSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDL 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTSENDFLVNCGTYMAHVTNDYFPAPNHRV-----KFVNAERLSLPFFLNGGHEAVIE- 293
                                                                                                                                                                                                      5 VPTFSLAEL-----QQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 VGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Streptomyces clavuligerus
Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 26-May-2000
Accession: A29894
                                                                                                                                                                    5 VPTFSLAELQQGLHQD-----EPRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHG
                                                                                                                                                                                                                                                                             59 SEAEK----RAVISPVPTMRRGFIGLESESTAQITNTGSYSDYSMCYSMGTADNLFP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 VPTIDISPLFGTDAAAKKRVAEEIHGACRGSGFFYATNHGV---DVQQLQDVVNEFHGAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.0%; Score 164; DB 2; Length 329;
Best Local Similarity 23.8%; Pred. No. 4.4e-07;
Matches 77; Conservative 50; Mismatches 150; Indels 46; Gaps
                                                                                                                 90;
                                                           Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 329;
7;48,212,268/Binding site: iron (His) #status predicted
                                                     10.8%; Score 176; DB 2;
llarity 24.5%; Pred. No. 3.6e-08;
Conservative 39; Mismatches 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : | : | : | : | DFVPE-GASEEVRNEALSYGDYL 315
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                                                        Query Match
Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101
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C,Superfamily: isopenicillin N synthase
C;Keywords: antibiotic biosynthesis; ascorbic acid; iron; metalloprotein; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isopenicillin N synthase (EC 1.14.11.-) pcbC {similarity} - Streptomyces griseus (strain
C,Species: Streptomyces griseus
C,Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 26-May-2000
C,Accession: A61155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Garcia-Dominguez, M.; Liras, P.; Martin, J.F.
Antimicrob. Agents Chemother. 35, 44-52, 1991
A;Title: Cloning and characterization of the isopenicillin N synthase gene of Streptomyo
                                                                                                                                                                                        deacetoxycephalosporin C synthetase 2 - Lysobacter lactamgenus (strain YK90)
C;Speciaes: Lysobacter lactamgenus
C;Speciaes: Lysobacter VK90
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-2000
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-2000
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-2000
C;Accession: S$4100
B;Kimura, H.; Izawa, M.; Miyashita, H.; Shimizu, Y.; Sumino, Y.; Suzuki, M.
submitted to the EMBL Data Library, October 1990
A;Description: Gene cluster involved in the cephalosporin biosynthesis from Lysobacter
A;Accession: S$4101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQ 2377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 VKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDW 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 NRMAPHYDLSIVSLILQTPCPNGFVSLQVEIDGRFVEVPPPRPGCVVVFCGSIAPLVSDGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 GSEAEKRAVISPVPTMRRGFIGLESESTAQITNIGSYSDYSMCYSMGTADNLFPSGDFGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X56660, NID:g769806; PIDN:CAA39985.1; PID:g769809
A;Experimental source: strain YK90
C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
C;Keywords: antibiotic biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 DTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKD----LVIDFFEH
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A;Molecule type: DNA
A;Residues: 1-329 <GAR>
A;Cross-references: GB:X54609; NID:g509097; PIDN:CAA38431.1; PID:g509098
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           avuligerus.
A;Reference number: A61155; MUID:91197089; PMID:1901702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 852; DB 2;
; Pred. No. 1.6e-69;
48; Mismatches 91;
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     GNYVNIRRTSKA 311
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GNYVNMRRDKPA 312
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Best Local Similarity 52.9°
Matches 165; Conservative
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A;Residues: 1-313 <KIM>
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C. Accession: D84713

R. Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A. Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A. Reference number: A84420; MUID: 20083487; PMID: 10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable gibberellin 20-oxidase T7P1.12 (imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C;Accession: D96635 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
                                                                                                                                                                                                                                                                   194 -----PLKLGPDGEKLSFEHHQDVSLITVLYQTAIPN----LQVETAEGYLDIPVSDE 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPEHGSEAEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMC7SWGTAD----N 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 FHEODSDVRKKFY------TRDVTKTVKYNSNFDLYSSPSANWRDTLS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 LFPSGDF------GRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEP- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 CPMAPDVPETEDLPDICGEIMLEYAKRVMKLGELIFELLSEALGLNPNHLKE--MDCTKG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LLRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLP 216
--NLFPS----GDFGRIW 119
                                                   -----YMAVEGKKANEŚFCYLNPSFDADHATIKAGLPSHEVNIWPDEARHPGMRRFY 139
                                                                                                                                                                       140 EAYFSDVFDVAAVILRGFAIALGRE-----ESFFERHFSMDDTLSAVSLIRYPFLENYP- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Cross-references: GB: AE002093; NID: 93201612; PIDN: AAC20719.1; GSPDB: GN00139
                                                                                                             TOYFDROYTASRAVAREVLRATGTEPDGGVEAF-----LDCEPLLRFRYFPQVPE
                                                                                                                                                                                                                              170 HRSAEEQPLRMAP------HYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPTFSLAELQQGLHQDEF------RRCLRDKGLFYLTDCGLTDTELKSAKDLVID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 YRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSV--FFLRP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 146.5; DB 2; Length 362;
; Pred. No. 1.9e-05;
40; Mismatches 118; Indels 67
                                                                                                                                                                                                                                                                                                                                                                                                      243 HFLVNCGTYMAHITNGYYPAPVHRV-----KYINAERLSIPFF 280
                                                                                                                                                                                                                                                                                                                                                  221 AVLVFCGAIATLVTGGQVKAPRHVAAPRRDQIAGSSRTSSVFF 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 2
C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable dioxygenase [imported] - Arabidopsis thaliana
79 GLESESTAQITNTGSYSDYSMCYSMGTAD-
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary A;Molecule type: DNA
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Subperfamily: isopenicillin N synthase
; Keywords: antibiotic biosynthesis; ascorbic acid; iron; metalloprotein; oxidoreductase
; 45, 209, 265/Binding site: iron (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΥK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :Keywords: antibiotic biosynthesis; ascorbic acid; iron; metalloprotein; oxidoreductase
;45,209,265/Binding site: iron (His) #status predicted
                                                                                                                                                                                                   Nucleic Acids Res. 18, 660, 1990
'Title: Nucleotide sequence of the isopenicillin N synthase gene (pcbC) of the gram neg
'Reference number: S08218; MUID:90174998; PMID:2308852
'Accession: S08218
                                                                                  (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .eopenicillin N synthase (EC 1.14.11.-) [similarity] - Lysobacter lactamgenus (strain ;Species: Lysobacter lactamgenus ,Variety: strain YK90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                      sopenicillin N synthase (EC 1.14.11.-) pcbC [similarity] - Flavobacterium sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----NLFPS----GDFGRIW 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 RCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEK-----RAVTSPVPTMRRGFT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 RACRGSGFFYAANHGV---DLAALQKFTTDWHMAMSAEEKWELAIRAYNPANPRNRNGY- 87
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v,Residues: 1-326 <KIM>
v,Eesidues: 1-326 <KIM>
v,Cross-references: EMBL:X56660, NID:g769806; PIDN:CAA39983.1; PID:g769807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 9.9%; Score 162; DB 2; Length 326; 1 Similarity 22.9%; Pred. No. 6.6e-07; 65; Conservative 34; Mismatches 107; Indels
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Best Local Similarity 22.9%; Pred. No. 6.6e-07;
Matches 65; Conservative 34; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 AVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFF 264
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Matches 65; Conserv
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- protein search, using sw model OM protein February 3, 2004, 17:33:57; Search time 42 Seconds (without alignments) 1175.332 Million cell updates/sec Run on:

score: Perfect

1637 1 MDTTVPTFSLAELQQGLHQD.....ATFQDWIGGNYVNIRRTSKA 311 US-09-582-486-1

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1107863 segs, 158726573 residues Searched:

1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_19Jun03:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Deacetoxycephalosp	S. clavuligerus wi	Streptomyces clavu	Streptomyces clavu	Streptomyces clavu	Streptomyces clavu	S. clavuligerus pe	S. clavuligerus pe	Expandase mutant R
	ID	AAY22220	AAW17775	AAU11044	AAU11050	AAU11046	AAU11051	AAU11053	AAU11525	AAW34168
	DB	20	18	23	23	23	23	23	23	18
	Match Length DB ID	311	311	311	311	311	311	310	310	311
Ouerv	Match	100.0	99.5	99.2	99.4	99.3	99.3	99.3	99.3	99.3
	Score	1637	1629	1629	1627	1626	1626	1625	1625	1625
Result	NO.	-	7	m -	4	Ñ	é	7	ω	б

Expandase mutant R	~	Streptomyces clavu	Streptomyces clavu		Expandase mutant R	Expandase mutant R	Streptomyces clavu	S. clavuligerus pe	Streptomyces clavu	Deacetoxycephalosp	Expandase mutant R	Expandase mutant R	Expandase mutant P	S. clavuligerus ex	ä	S. clavuligerus pe	. clavuligerus	. clavuligerus p	. clavuligerus p			Ω	··			Expandase mutant C				S. clavuligerus ex	. clavuli				S. clavuligerus ex
AAW34176	AAW34175	AAE12016	AAU11047	ABG73769	AAW34167	AAW34177	AAU11048	AAU11528	AAU11052	AAP93215	AAW34166	AAW34169	AAW34174	AAW40424	AAU11049	AAU11054	AAU11526	AAU11531	AAU11532	AAU11533	AAU11534	AAU11535	AAW34171	AAW34173	AAW34170	AAW34172	AAU11529	AAU11521	AAU11527	AAW40425	AAW40426	AAW40428	AAW40429	AAU11530	AAW40427
18	18		23	24	18	18	23	23	23	10	18	18	18	19	23	23	23	23	23	23	23	23	18	18	18	18	23	23	23	19	19	19	19	53	19
311	311	311	311	311	311	311	311	310	311	311	311	311	311	311	311	309	309	310	310	310	310	310	311	311	311	311	309	308	308	311	311	311	311	0	311
99.3	99.5	99.2	99.2	9	99.1	99.1	99.1	99.1	99.1	σ	6	99.0	σ	σ	6	99.0	0.66	9.	σ	99.0	0.66	0.66	0.66	99.0	98.9	8	8	98.7	98.7	œ.	æ,	œ	æ,	٠	8
1625	1624	1624	1624	1624	1623	1623	1623	1622	1622	1621	1621	1621	1621	1621	1621	1620	1620	1620	1620	1620	1620	1620	1620	1620	1619	1619	1617	1616	1616	1616	1615	1614	1614	1613	1612
10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAY22220 standard; protein; 311 AA Deacetoxycephalosporin C synthase. (first entry) 16-SEP-1999 AAY22220; AAY22220

DAOCS; deacetoxycephalosporin C synthase; antibacterial production; three-dimensional crystal structure; beta-lactam production; penicillin; cephalosporin; cepham; 2-oxoglutarate dependent enzyme; inhibitor; fibrotic disease; liver cirrhosis; arthritis; genetic disorder; therapy; 98GB-0013644. 97GB-0027370. 98WO-GB03860 Streptomyces clavuligerus. herbicide resistance. WO9933994-A1. 24-DEC-1998; 24-JUN-1998; 24-DEC-1997; 08-JUL-1999

Baldwin JE, Hajdu J, Harlos K, Lloyd MD; Roach PL, Schofield CJ, Terwisscha Van Scheltinga AS; Andersson I, Ramaswamy S, Valegard K;

(ISIS-) ISIS INNOVATION LTD.

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The invention relates to three-dimensional crystal structures of
deacetoxycephalosporin C (DAOC) synthase (DAOCS), which has this amino
acid sequence. Micro-organisms capable of expressing a gene encoding a
caid sequence. Micro-organisms capable of expressing a gene encoding a
modified DAOCS are useful for the production of beta-lactams of the
penicillin or cephalosporin (including cepham) families. The 3D structure
of DAOCS is used to determine or predict the structure of another related
2-oxoglutarate dependent enzyme (such as deacetylcephalosporin C synthase
CC 2-oxoglutarate dependent enzyme (such as deacetylcephalosporin C synthase
CC c coxyme or for designing an inhibitor for the omodify the other
cenzyme may be prolyl 4/3 or aspartyl/lysyl-hydroxylase and the inhibitor
cenzyme may be prolyl 4/3 or aspartyl/lysyl-hydroxylase and the inhibitor
cenzyme may be prolyl 4/3 or aspartyl/lysyl-hydroxylase and the inhibitor
certain genetic disorders. Alternatively, the other enzyme may be
p-hydroxyphenylpyruvate dloxygenase and the inhibitor used to treat
certain genetic disorders. Alternatively, the other enzyme may be
prolycide resistance and the information is used to design new herbicides
to overcome the problem of resistance. The crystal structure data allows
commercially valuable antibacterial materials, or to enable the modified
cenzyme to produce unnatural (e.g. exponethylene cephams) or optimise the
production of minor products (e.g. albeta-hydroxycephams) for use as
antibacterials
commercials
                                                                           al crystal structures of deacetoxycephalosporin C for the production of beta-lactams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or commercially valuable compounds.
                                                                                                                                                            Claim 1; Page 11; 178pp; English
                                                                              Three-dimensional crystal
                         WPI; 1999-405515/34
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Sequence

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120
                                                                                                                           APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA 240
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                                                                      1 MDTTVPTFSLAELQQQLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLV1DFFEHGSE
                                                                                                                                                                                                                                     APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
                                                                                                                                                                                                                                                                                        PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG
                                                                                                           61 AEKRAVTSPVPIMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWT
                                                      1 MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE
                             Gaps
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 100.0%; Score 1637; DB 20; Length 311; 100.0%; Pred. No. 1.1e-172; cive 0; Mismatches 0; Indels 0;
Query Match
Best Local Similarity 100.
Matches 311, Conservative
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S. clavuligerus wild type expandase.
            AAW17775 standard; protein; 311
                                                   (first entry)
                                                   17-FEB-1998
                              AAW17775;
AAW17775
ID AAW
XX
AC AAW
XX
DT 17-
XX
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RESULT 2

301 NYVNIRRTSKA 311

Expandase, 7-aminodesacetoxycephalosporanic acid, 7-ADCA production, thiazolidine ring expansion, penicillin N, dihydrothiazine ring, enzyme; semi-synthetic cephalosporin production, penicillin G, isopenicillin N, 95EP-0203259. 95US-0007564 96WO-EP05358 Streptomyces clavuligerus KONN) GIST-BROCADES BV. cephalosporin ring; DOAC UNIV OXFORD 27-NOV-1996; 27-NOV-1995; WO9720053-A2 27-NOV-1995; 05-JUN-1997. UYOX-)

Expandase enzymes with mutation(s) to alter substrate specificity used particularly for production of 7-amino:desacetoxy:cephalosporanic acid Van Der Laan JM; Bovenberg RAL, Sutherland JD, WPI; 1997-310608/28.

Disclosure, Fig 1; 21pp; English

This sequence represents the wild type expandase from Streptomyces clavuligerus. The DNA encoding this sequence was subjected to site directed mutagenesis to create the mutant expandase sequences of the invention (see AAW34166-W3417). The mutant expandase sequences of the altered substrate specificity compared to the wild type expandase. Expandase catalyses the expansion of the 5-membered thiazolidine ring of penicillin N to the 6-membered dihydrothiazine ring of DOAC. The mutant expandase gene is used particularly for the production of 7-aminodesacetoxycephalosporanic acid (7-ADCA). 7-ADCA is one of the key intermediates that is used in the preparation of semi-synthetic cephalosporins. The mutant expandases have improved ability to expand penicillin G into a cephalosporin ring in vitro and/or in vivo where other penicilling such as penicillin N and isopenicillin N can act as competing substrates.

311 AA; Sequence

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                                                                                                                                                                                                                                                                                                       121 ÖYFDRÖYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRM 180
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                                                                                       1 MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE
                                                                                                               1 MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE
                                                                                                                                                                            61 AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWT
                                                                                                                                                                                                                                                               QYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRM
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                                            0; Gaps
Query Match 99.5%; Score 1629; DB 18; Length 311; Best Local Similarity 99.7%; Pred. No. 8.5e-172; Matches 310; Conservative 0; Mismatches 1; Indels 0
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121 QYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRM 180
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEKRAVISPVPIMRRGFIGLESESTAQIINIGSYSDYSMCYSMGTADNLFPSGDFERIWT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New enzyme useful for ring-expanding penicillin G to produce phenylacetyl-7-amino desacetoxycephalosporanic acid, comprises penicillin expandase having increased specificity for substrates such as penicillin G -
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                                                                                                                                                                                                                                                                                                       Penicillin N expandase; ring-expanding; penicillin G;
phenylacetyl-7-ADCA; amino desacetoxycephalosporanic acid;
cephalosporin; cephalexin; penicillin V.
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                                                                                                                    AAU11044 standard; Protein; 311 AA
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                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces clavuligerus.
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301 NYVNIRRISKA 311
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                                                                                                                                                                 AAU11044;
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The present invention relates to new penicillin expandases modified to improve the ring-expanding activity for a substrate which is not the atural_aubertaffe of Fife Unmodified expandase. The invention is not useful for ring-expansion of penicillin of to produce phenylacetyl-7-ADCA (amino desacetoxycephalosporanic acid) and the phenylacetyl side chain is removed from phenylacetyl-7-ADCA to produce 7-ADCA, which is useful as a starting point for the production of a range of semi-synthetic caphalosporins, most notably cephalexin. The polymucleotide of the invention is useful for producing a primer e.g. a PCR primer and as a primer solution of the penicillin of a probe. The modification of the penicillin of or y as a substrate. The modified expandase has enhances the activity of the enzyme such as penicillin of or y as a substrate. The modified expandase has enhanced catalytic activity or increased specificity for another substrate such as cativity or increased specificity for another substrate such as clavility of This sequence is one of a collection of Streptomyces clavuligerus mutents, AAU11054 and AAU11521-AAU1537, used in the invention to improve the ring-expanding activity of expandase.
                                                                                                                                                                                           241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
                                                                                                                                        241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
181 APHYDLSMYTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
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phenylacetyl-7-ADCA; amino desacetoxycephalosporanic acid;
cephalosporin; cephalexin; penicillin V; mutant; mutein.
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The present invention relates to new penicillin expandases modified to improve the ring-expanding activity for a substrate which is not the neutral substrate of the unmodified expandase. The invention is useful for ring-expansion of penicillin G to produce phenylacetyl-7-ADCA (amino desacetoxycephalosporanic acid) and the phenylacetyl-7-ADCA to produce 7-ADCA, which is useful as a starting point for the production of a range of semi-synthetic cephalosporins, most notably cephalexin. The polynucleotide of the invention is useful for producing a primer e.g. a PCR primer and as a probe. The modification of the penicillin expandase enhances the activity of the enzyme such as penicillin Nexpandase for penicillin G or V as a substrate. The modified expandase has enhanced catalytic activity or increased specificity for another substrate such as penicillin G. This sequence is one of a collection of Streptomyces clavuligerus mutants, AAU11046-AAU11054 and AAU11521-AAU11537, used in the invention to improve the ring-expanding activity of expandase.

CC but is derived from the Streptomyces clavuligerus wild-type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFERIWT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              penicillin N expandase sequence given in figure 1 (see AAU11044)
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phenylacetyl-7-ADCA; amino desacetoxycephalosporanic acid;
cephalosporin; cephalexin; penicillin V; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1626; DB 23;
Pred. No. 1.8e-171;
1; Mismatches 1;
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                                               Claim 6; Page -; 42pp; English.
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Best Local Similarity 99.4%;
Matches 309; Conservative
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as penicillin G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRHHVAAPRROQIAGSGRISSVFFLRPNADFIFSVPLARECGFDVSLDGETATFQDMIGG 300
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                                                                                                                                                                                                                                              1 MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE
  present protein sequence is not shown in the specification
                                                                                                                                                                                            Gaps
                      but is derived from the Streptomyces clavuligerus wild-type
penicillin N expandase sequence given in figure 1 (see AAU11044)
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                                                                                                                                               Length 311;
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phenylacetyl-7-ADCA; amino desacetoxycephalosporanic acid;
cephalosporin; cephalexin; penicillin V; mutant; mutein.
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                                                                                                                                                                                            Indels
                                                                                                                                             Score 1627; DB 23;
Pred. No. 1.4e-171;
1; Mismatches 1;
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Misc-difference 158
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                                                                                                                                             Query Match
Best Local Similarity 99.4%;
Matches 309; Conservative
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nyvnlærfska
                                                                                                311 AA;
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RESULT 5
AAU11046
AAU11046
AAU11046
AAU11046
AAU11046
AAU11046
AAU1104

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Gaps

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Indels

Length 311;

120

9 9

240 240

180

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improve the ring expanding activity for a substrate which is not the natural substrate of the unmodified expandase. The invention is useful for ring-expansion of penicillin G to produce phenylacetyl-7-ADCA (amino desacetoxycephalosporanic acid) and the phenylacetyl-7-ADCA (amino desacetoxycephalosporanic acid) and the phenylacetyl-7-ADCA (amino desacetoxycephalosporanic acid) and the phenylacetyl-7-ADCA (as a range of semi-synthetic cephalosporins, most notably cephalexin. The polymucleotide of the invention is useful for producing a primer e.g. a PCR primer and as a probe. The modification of the penicillin N expandase enhanced the activity of the enzyme such as penicillin N expandase for penicillin G or V as a substrate. The modified expandase has enhanced catalytic activity or increased specificity for another substrate such as penicillin G. This sequence is one of a collection of Streptomyces clavuligerus mutants, AAU11046-AAU11054 and AAU11521-AAU1157, used in the invention to improve the ring-expanding activity of expandase.

Note: The present protein sequence is not shown in the specification of but is derived from the Streptomyces clavuligerus wild-type.
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                                                                                                                                                                                                                                                                                                                          New enzyme useful for ring-expanding penicillin G to produce phenylacetyl-7-amino desacetoxycephalosporanic acid, comprises penicillin expandase having increased specificity for substrates such as penicillin G -
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                /note= "Wild-type Ile substituted by Met"
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1; Mismatches 1;
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                                                                                                                                   09-MAY-2001; 2001WO-GB02047.
                                                                                                                                                                        09-MAY-2000; 2000GB-0011185.
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Matches 309; Conservative
                                                                                                                                                                                                                                                        Johnson RI, Newbert RW;
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301 NYVNMRRTSKA 311
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Misc-difference 305
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The present invention relates to new penicillin expandases modified to improve the ring-expanding activity for a substrate which is not the natural substrate of the unmodified expandase. The invention is useful for ring-expansion of penicillin G to produce phenylacetyl-7-ADCA (amino desacetoxycephalosporanic acid) and the phenylacetyl side chain is removed from phenylacetyl-7-ADCA to produce 7-ADCA, which is useful as a starting point for the production of a range of semi-synthetic cephalosporins, most notably cephalexin. The polynucleotide of the invention is useful for producing a primer e.g. a PCR primer and as a privent of the penicillin N expandase enhances the activity of the enzyme such as penicillin N expandase has enhanced catalytic activity of increased specificity for another substrate such as penicillin G or V as a substrate. The modified expandase has enhanced catalytic activity of increased specificity for another substrate such as penicillin G or V as a substrate. The modified expandase has enhanced catalytic cativity or increased specificity for another substrate such as penicillin G or V as a substrate and another of a collection of Streptomyces clavuligerus mutants, AAUI1064-AAUI1054 and AAUI1521-AAUI137, used in the invention to improve the ring-expanding activity of expandase.

Note: The present protein sequence is not shown in the specification but is derived from the Streptomyces clavuligerus wild-type

    S. clavuligerus penicillin N expandase 1 residue deletion at C-terminus.

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phenylacetyl-7-ADCA; amino desacetoxycephalosporanic aci
cephalosporin; cephalexin; penicillin V; mutant; mutein.
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Pred. No. 2.3e-171;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                       AAU11053 standard; Protein; 310 AA
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                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                         Streptomyces clavuligerus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnson RI, Newbert RW;
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Best Local &
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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to new penicillin expandases modified to improve the ring-expanding activity for a substrate which is not the natural substrate of the unmodified expandase. The invention is useful for ring-expansion of penicillin G to produce phenylacetyl-7-ADCA (amino desacetoxycephalosporanic acid) and the phenylacetyl side chain is removed from phenylacetyl-7-ADCA to produce 7-ADCA, which is useful as a starting point for the production of a range of semi-synthetic cephalosporins, most notably cephalexin. The polymucleotide of the invention is useful for producing a primer e.g. a PCR primer and as
                                                                                                                                           APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
                                                                                                                          APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
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phenylacetyl-7-ADCA; amino desacetoxycephalosporanic aci
cephalosporin; cephalexin; penicillin V; mutant; mutein.
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a probe. The modification of the penicillin expandase enhances the activity of the enzyme such as penicillin N expandase for penicillin of or V as a substrate. The modified expandase has enhanced catalytic activity or increased specificity for another substrate such as penicillin G. This sequence is one of a collection of Streptomyces clavuligerus mutants, AAU11046-AAU11054 and AAU11521-AAU11537, used in the invention to improve the ring-expanding activity of expandase. Note: The present protein sequence is not shown in the specification but is derived from the Streptomyces clavuligerus wild-type penicillin N expandase sequence given in figure 1 (see AAU11044).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE
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                                                                                                                                                                                                               Length 310;
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                                                                                                                                                                                                              Query Match 99.3%; Score 1625; DB 23; Best Local Similarity 99.7%; Pred. No. 2.3e-171; Matches 309; Conservative 0; Mismatches 1;
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Synthetic.
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27-NOV-1995;
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                                                                                                                                                                                    Sequence
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AAW34168
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cephalosporin ring; DOAC; mutant
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                                                                                                                                                                       AAW34166-W34177 represent mutant expandase sequences of the invention.

These sequences represent mutated versions of the Streptomyces

Calavuligerus expandase sequences shown in AAW1775. The DNA encoding the
wild type expandase was subjected to site directed mutagenesis to create
these sequences. The mutant expandase sequences have an altered

Combertate specificity compared to the wild type expandase. Expandase

Combertate specificity compared to the wild type expandase. Expandase

Comparizor to the 5-membered thiazolidine ring of penicillin

N to the 6-membered dihydrothiazine ring of DOAC. The mutant expandase

Comparizor the production of

T-aminodesacetoxycephalosporanic acid (7-ADCA). 7-ADCA is one of the key
intermediates that is used in the preparation of semi-synthetic

Comparizor the sequences have improved ability to expand

Competing substrates.

Competing substrates.
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                                                                                              Expandase enzymes with mutation(s) to alter substrate specificity
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                                                                                                                                                                                                                                                                                                                                                                                                                             99.3%; Score 1625; DB 18; Length 311; 99.4%; Pred. No. 2.4e-171; ive 1; Mismatches 1; Indels 0
                                         Van Der Laan JM;
                                                                                                         used particularly for production of 7-amino:desacetoxy:cephalosporanic acid
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                                                                                                                                                   Claim 2; Page -; 21pp; English.
                                        Sutherland JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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GIST-BROCADES BV UNIV OXFORD.
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                                         Bovenberg RAL,
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 ( KONN
              (nxox-)
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ID AAW3
XX AC AAW3
XX DT 17-F
DT 17-F
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XX EXPA
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AAW34166-W34177 represent mutant expandase sequences of the invention. These sequences represent mutated versions of the Streptomyces clavuligerus expandase sequences shown in AAW17775. The DNA encoding the wild type expandase was subjected to site directed mutagenesis to create these sequences. The mutant expandase sequences have an altered substrate specificity compared to the wild type expandase. Expandase catalyses the expansion of the S-membered thiazolidine ring of penicillin N to the 6-membered dibydrothiazine ring of DOAC. The mutant expandase gene is used particularly for the production of 7-ADCA). 7-ADCA is one of the key intermediates that is used in the preparation of semi-synthetic cephalosporins. These sequences have improved ability to expand penicilling such as penicillin N and isopenicillin N can act as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRHHVAAPRRDQIAGSSKTSSVFFLRDNADFTPSVPLARECGFDVSLDGETATFQDWIGG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRHHVAAPRRDQIAGSSRTSSVFFLQPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expandase enzymes with mutation(s) to alter substrate specificity used particularly for production of 7-amino:desacetoxy:cephalosporanic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovenberg RAL, Sutherland JD, Van Der Laan JM;
                                                                                                                                                              /note= "Arg to Gln mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0007564
95EP-0203259
                                                                                                                                                                                                                                                                                                                                                               96WO-EP05358
Streptomyces clavuligerus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KONN ) GIST-BROCADES BV. (UYOX-) UNIV OXFORD.
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Matches 309; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 AA;
                                                                                                                            Misc-difference
                                                                                                                                                                                                                            WO9720053-A2
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241 PRHHVAAPRRDQIAGSSRTSSVFFLNPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
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1 MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE
                                                                                    OYFDROYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPOVPEHRSAEEQPLRM
                                                                                                                                           APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
                                                                                                                                                                                                                                                            NYVNIRRTSKA 311
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NYVNIRRTSKA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                        AAE12016;
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                                                                                                                                                                                                                  Expandase; 7-aminodesacetoxycephalosporanic acid; 7-ADCA production; thiazolidine ring expansion; penicillin N; dihydrothiazine ring; enzyme; semi-synthetic cephalosporin production; penicillin G; isopenicillin N; cephalosporin ring; DOAC; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expandase enzymes with mutation(s) to alter substrate specificity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1624; DB 18;
Pred. No. 3e-171;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Van Der Laan JM;
                                                                                                                                                                                                                                                                                                                                                               /note= "Arg to Asn mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used particularly for production of 7-amino:desacetoxy:cephalosporanic acid
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                                                                                                   AAW34175 standard; protein; 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.2%;
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95EP-0203259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-EP05358
                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                        Streptomyces clavuligerus.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KONN ) GIST-BROCADES BV (UYOX-) UNIV OXFORD.
                    Expandase mutant R266N
 NYVNIRRTSKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              competing substrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-310608/28
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Best Local Similarity
Matches 309; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 AA;
                                                                                                                                                                                                                                                                                                                                                Misc-difference
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oxygenase; non-haeme iron [II) dependent family; oxidase; mutant; mutein.
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                                                                                                  Streptomyces clavuligerus modified deacetoxycephalosporin C synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Method for producing antibiotics, particularly penicillin G or V, comprises employing a modified isopenicillin N synthethase, in either an organism or a cell-free system under the control of bicarbonate
                                                                                                                                 Deacetoxycephalosporin C synthetase, DAOCS; antibiotic; penicillin;
                                                                                                                                                                                                                                                                         /note= "Wild type Ala substituted with Arg"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Warner
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                                                                                                                                                                                                                                       Location/Qualifiers
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AAE12016 standard; Protein; 311 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kadyrzhanova DK,
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                                                                  (first entry)
                                                                                                                                                                                      Streptomyces clavuligerus
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                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                 06-OCT-1999;
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                                                                    18-DEC-2001
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Indels

0; Mismatches

Conservative

MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE

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as penicillin G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
                                                                                                                                                                                                                                                                  9
on bicarbonate to make the antibiotic. The present sequence is Streptomyces clavuligerus modified deacetoxycephalosporin C synthetase showing an Arg181 in place of Ala181.
                                                                                                                                                                                                                                                    MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLV1DFFEHGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 RPHYDLSMYTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APHYDLSMYTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRHHVAAPRRDQIAGSSRTSSVPFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New enzyme useful for ring-expanding penicillin G to produce phenylacetyl-7-amino desacetoxycephalosporanic acid, comprises penicillin expandase having increased specificity for substrates such
                                                                                                                                                                                                                        1 MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE
                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces clavuligerus penicillin N expandase L158A mutant
                                                                                                                               99.2%; Score 1624; DB 22; Length 311; 99.4%; Pred. No. 3e-171; 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penicillin N expandase; ring-expanding; penicillin G;
phenylacetyl-7-ADCA; amino desacetoxycephalosporanic acid;
cephalosporin; cephalexin; penicillin V; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild-type Leu substituted by Ala"
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Synthetic.
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                                                                                                                                                      Best Local Similarity 99.4 Matches 309, Conservative
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                                                                                         311 AA;
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The present invention relates to new penicillin expandases modified to improve the ring-expanding activity for a substrate which is not the natural substrate of the unmodified expandase. The invention is useful for ring-expansion of penicillin G to produce phenylacetyl-7-ADCA (amino desacetoxycephalosporanic acid) and the phenylacetyl side chain is removed from phenylacetyl-7-ADCA (arange of semi-synthetic cephalosporins, most notably cephalexin. The polynucleotide of the invention is useful for producing a primer e.g. a PCR primer and as a probe. The modification of the penicillin expandase enhances the activity of the enzyme such as penicillin expandase for penicillin cortivity or increased specificity for another substrate such as penicillin G. This sequence is one of a collection of Streptomyces clavity or increased specificity for another substrate such as penicillin G. This sequence is one of a collection of Streptomyces clavuligerus mutants, AMUII046-AMUII054 and AMUII521-AMUII531, used in the invention to improve the ring-expanding activity of expandase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            penicillin N expandase sequence given in figure 1 (see AAU11044).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 99.2%; Score 1624; DB 23; Length 311; Best Local Similarity 99.4%; Pred. No. 3e-171; Matches 309; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           but is derived from the Streptomyces clavuligerus wild-type
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Examples; Page -; 42pp; English.
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                                                                                                                                                                                                                   This invention describes a novel enzyme of a non-heme iron II dependent family of oxygenases and oxidases which is in a pathway to produce an antibiotic. The enzyme comprises a mutation which is an amino acid residue that is two amino acid residues upstream of a histidine residue which is an iron ligand of the enzyme, where the mutation renders the enzyme dependent on bicarbonate to produce the antibiotic. The enzyme and modified organisms containing the enzyme are useful for producing an antibiotic such as peniciallin G or V and cephalosporin C. This sequence represents an deacetoxycephalosporin C synthetase (DAOCS) variant the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWT 120
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                                                                                                                                                                                                                                                                                                                                                               Length 311;
                                                                                                                                                    Novel enzyme of non-heme iron II dependent family of oxyge oxidases useful for producing antibiotic, has mutation the enzyme dependent on bicarbonate to produce the antibiotic
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Pred. No. 3e-171;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                             99.2%;
                                                                                                           Kadyrzhanova DK,
                                            08-AUG-2001; 2001US-0924841.
                                                                99US-0413231
                                                                                      (UNMS ) UNIV MICHIGAN STATE
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Matches 309; Conservative
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                                                                                                                                WPI; 2003-147393/14.
                                                                                                                                                                                                                                                                                                                                          311 AA;
US2002127633-A1
                                                                06-OCT-1999;
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                      12-SEP-2002
                                                                                                           Dilley DR,
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These sequences represent mutated versions of the Streptomyces clavuligerus expandase sequences shown in AAW1775. The DNA encoding the wild type expandase was subjected to site directed mutagenesis to create these sequences. The mutant expandase sequences have an altered substrate specificity compared to the wild type expandase. Expandase catalyses the expansion of the 5-membered thiazolidine ring of penicillin N to the 6-membered dihydrothiazine ring of DOAC. The mutant expandase gene is used particularly for the production of 7-aminodesacetoxycephalosporanic acid (7-ADCA). 7-ADCA is one of the key intermediates that is used in the preparation of semi-seynthetic cephalosporins. These sequences have improved ability to expand penicillin G into a cephalosporin ring in vitro and/or in vivo where other penicilling such as penicillin N and isopenicillin N can act as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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thiazolidine ring expansion; penicillin N; dihydrothiazine ring; enzyme; semi-synthetic cephalosporin production; penicillin G; isopenicillin N; cephalosporin ring; DOAC; mutant.
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                                                                                                                                                                                                                                                                                                                       /note= "Arg to Met mutation"
                                                                                                                                                                                                                                     Location/Qualifiers
74
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                                                                                                                                                        Streptomyces clavuligerus
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Matches 309; Conserv
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                                                                                                                                                                                                                                                      Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-1995;
27-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-1997
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241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300

301 NYVNIRRTSKA 311 ||||||||||| 301 NYVNIRRTSKA 311

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Search completed: February 3, 2004, 17:36:36 Job time: 43 secs

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6

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                 Copyright
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OM protein - protein search, using sw model

February 3, 2004, 17:33:58; Search time 17 Seconds (without alignments) 860.312 Million cell updates/sec

Run on:

US-09-582-486-1

score: Title: Perfect

1637 1 MDTTVPTFSLAELQQGLHQD.....ATFQDWIGGNYVNIRRTSKA 311 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES		
Result No.	Score	Owery Match	Length	DB	ID	Description	ption
	1629	. 6	311	-	CEFE STRCL	P18548	streptomyce
7	1186.5	72.5	314	Н	CEFE_NOCLA	003047	nocardia
m	w	φ.	310	Н	CEFF_NOCLA	P42219	nocardia la
4	939.5	7.	318	-1	CEFF STRCL	P42220	B
ß	\sim	9.95	332	-	EXPA CEPAC	P11935	c cephalosp
9	179	ö	329	-	IPNS_STRJU	P18286	g
7	176	ö	329	-	I PNS STRGR	054243	
œ	164	°.	329	Н	IPNS_STRCL	P10621	
0,	162	•	326	-	I PNS FLASS	P16020	
10	162	•	326	-	IPNS_LYSLA	048739	lysobacter
11	143	•	333	Ч	IPNS_STRLP	P12438	
12	140	•	348	-	FLS PETHY	007512	petunia hyb
13	138	8.4	328	-	IPNS NOCLA	P27744	
14	137.5	8.4	335	-		65wz60	citrus unsh
15	137	8.4	321	Н	IPNS STRCT	053932	streptomyce
16	134.5		349	ч	rn	041452	solanum tub
17	133.5		331	-	I PNS PENCH	P08703	penicillium
18	127	•	334	٦	FLS EUSGR	Q9m547	
19	122.5	7.5	331	Н	IPNS EMENI	P05326	emericella
50	121		356	ч	LDOX_ARATH	096323	
21	118	•	365	Н	FL3H_DIACA	005964	
22	113.5		337	Н	FLS MALDO	Q9xhg2	_
23	110		. 397	-	ISP7 SCHPO	P40902	
24	109		336	-	FLS1_ARATH	096330	
25	108	9.9	356	-	FL3H_CALCH	005963	
56	106	٠	338	-	IPNS_CEPAC	P05189	
27	o	٠	395	-	LDOX MAIZE	P41213	zea mays (m
28	103.5	٠	430	-	LDOX PETHY	P51092	petunia hyb
29	101	٠	357	Н	LDOX MALDO	P51091	malus domes
30	66	٠	358	-1	FL3H_ARATH	098818	arabidopsi
31	96	٠	357	-	FL3H_MATIN	005965	
32	96	•	364	7	FL3H_MALDO	006942	malus domes

Pfam, PP03171; 20G-FeII Oxy; I. PROSITE; PS00185; IPNS I; FALSE_NEG. PROSITE; PS00186; IPNS 2; 1. Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin C;

3D-structure

004395 matthiola

1 FLS MATIN

291

5.8

95.5

33

EWBL; M.532-8; A.532-12.

PUR; T52312; T52312.

PDB; IDCS; 08-JUN-99.

PDB; IESH; 26-JUL-01.

PDB; IESH; 23-NOV-01.

PDB; IHJF; 01-JUN-01.

PDB; IRXF; 08-JUN-99.

PDB; IRXG; 08-JUN-99.

PDB; IRXG; 08-JUN-99.

PDB; IRXG; 08-JUN-99.

InterPro; IPR0020512; ZOG-FeII Oxy.

EMBL; M32324; AAA26715.1; -.

P33212 rhizobium f P55712 rhizobium s	Q9ryyl deinococcus P24397 hyoscyamus	P51093 vitis vinif Q07353 petunia hyb	P10967 lycopersico P46550 caenorhabdi		P22248 azotobacter Q8trk8 methanosarc
NOLW RHIFR NOLW RHISN	THIG DEIRA HY6H HYONI	LDOX_VITVI FL3H_PETHY	ACC3_LYCES TCPZ_CAEEL	FL3H ⁻ HORVU FL3H ⁻ VITVI	GLNA_AZOVI KPRS_METAC
234	267	362 369	363 539	377	467 283
9.0	5.5	5.5	ນ ນ ນ ນ	5.3	5.3
91.5	90.5	90.5	89.5 89.5	89 87	86.5 85.5
34	36	3 8	4041	42	44 45

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATCC 27064 / DSM 738 / NRRL 3585;
MRDLINE=89123150; PubMed=2644235;
Kovacevic S., Weigel B.J., Tobin M.B., Ingolia T.D., Miller J.R.;
"Cloning, characterization, and expression in Escherichia coli of streptomyces clavuligerus gene encoding deacetoxycephalosporin C
                                                                                                                                                                                                                                                                                                                                                                                                       cephalosporin C.
-!- CATALYTIC ACTIVITY: Penicillin N + 2-oxoglutarate + O(2) = deacetcxycephalosporin C + succinate + CO(2) + H(2)O.
-!- COFACTOR: Iron and ascorbate.
-!- PATHWAY: Cephalosporin antibiotics biosynthesis.
-!- SMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF OXIDOREDUCTASES. STRONG, TO CEFF.
                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol, 171:754-760(1989).
-!- FUNCTION: Catalyzes the step from penicillin N to deacetoxy-
                                                                                                                                                      Streptomyces clavuligerus.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1901;
                                                                              01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Deacetoxycephalosporin C synthetase (EC 1.14.20.1) (DAOCS)
                                  311 AA
                                  PRT;
                                                                01-NOV-1990 (Rel. 16, Created)
                                 STANDARD;
                                                                                                                                    (Expandase).
                                 STRCL
                                             P18548;
RESULT 1
CEFE_STRCL
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120

9 62

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52;

DB 1; Length 314;

122

180 182 240 300

encoding

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EMBL; Z13974; CAA78376.1; -.

PIR, S30900; S30900

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 PKHHVAAPGADKRVGSSRTSSVFFLRPNGDFRFSVPRARECGFDVSIPAETATFDDMIGG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 DYFARMYRASQDVARQVLTSVGAEPEVGMDAFLDCEPLLRLRYFPEVPEDRVAEEQPLRM
                                                                                                                                                                                                                                                                                                                                                                         61 AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 QYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 APHYDLSIVTLIHQTPCANGFVSLQVEVDGSYVDIPAQPGAVLVFCGAVATLVADGAIKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG
                                                                                                                                                                                                                                                                                                                                         2 DITVPIFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGL-TDTELKSAKDLVIDFFEHGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Deacetoxycephalosporin C hydroxylase (EC 1.14.11.-)
(Deacetylcephalosporin C synthetase) (DACS) (Beta-lactam hydroxylase)
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-!- SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
OXIDOREDUCTASES. STRONG, TO CEFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=96287477; PubMed=8703431;
Coque J., Engulta F.J., Cardoza R.E., Martin J.F., Liras P.;
"Characterization of the ceff gene of Nocardia lactamdurans a 3'-methylcephem hydroxylase different from the 7-cephem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                           PERMIT PRO3171, 20G-FeII OXY; I. T. PROSITE: PRO118; PROSITE: PRO118; PROSITE; PRO1086; INNS 1; FALSE NEG. PROSITE; PRO1086; INNS 2; FALSE NEG. Antibicatio blosynthesis; Oxidoreductase; Iron; Vitamin C. SEQUENCE 314 AA; 34530 MW; D007AD3DE67AlBDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appl. Microbiol. Biotechnol. 44:605-609(1996).
-!- FUNCTION: HYDROXYLATION OF DESACETOXICEPHALOSPORIN 3'POSITION TO FORM DEACETYLCEPHALOSPORIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis
NCBL_TaxID=1913;
                                                                                                                                                                                                                       72.5%; Score 1186.5; DB 1
69.8%; Pred. No. 3.6e-102;
ive 41; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310
                    synth.
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InterPro; IPR005123; 20G-FeII_Oxy
                       IPR002057; Isopen_N_
1171; 20G-FeII Oxy; 1
                                                                                                                                                                                                                                                    Best Local Similarity 69.8
Matches 217; Conservative
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                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                QYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRM 180
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                                                                                                                                                                      1 MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE
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SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Gen. Genet. 236:453-458(1993).
FUNCTION: Catalyzes the step from penicillin N to deacetoxy-
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MEDLINE=93173127; PubMed=8437592;
Coque J.J.K., Martin J.F., Liras P.;
Coque J.J.K., Martin J.F., Liras P.;
Characterization and expression in Streptomyces lividans of ceft genes from Nocardia lactamdurans: the organization of the cephamycin gene cluster differs from that in Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cephalosporin C.
CATALYTIC ACTIVITY: Penicillin N + 2-oxoglutarate + O(2)
deacetoxycephalosporin C + succinate + CO(2) + H(2)O.
COFACTOR: Iron and ascorbate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
                                                       Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Deacetoxycephalosporin C synthetase (EC 1.14.20.1) (DAOCS)
                                                                                                              Indels
34555 MW; 9C64ElFC37F524BC CRC64;
                                                    Score 1629; DB 1;
Pred. No. 4.4e-143;
0; Mismatches 1;
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                                                    Query Match
Best Local Similarity 99.7%;
Matches 310; Conservative
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  311 AA;
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Mol. Gen. Gen
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  SEQUENCE
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us-09-582-486-1.rsp

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PIR; A39204; A39204.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 YFDSLÝRAAQETARLVLTAAGÍYDGEDLDTLLDČDPVLRLRÝFPEVPEHŘAAEYEPRRMA 181
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Deacetoxycephalosporin C hydroxylase (EC 1.14.11.-)
(Deacetylcephalosporin C synthetase) (DACS) (Beta-lactam hydroxylase).
                                                                                                                                                                                                                                                                        DITVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91100311; PubMed=1987130;
Kovacevic S., Miller J.R.;
"Cloning and sequencing of the beta-lactam hydroxylase gene (ceff)
from Streptomyces clavuligerus: gene duplication may have led to
separate hydroxylase and expandase activities in the actinomycetes.";
J. Bacteriol. 173:398-400(1991).
-I- FUNCTION: HYDROXYLATION OF DESACETOXICEPHALOSPORIN C IN
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3'POSITION TO FORM DEACETYLCEPHALOSPORIN C. PATHWAY: CEPABLOSPORIN DIOSPYTATHORIS. SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF OXIDOREDUCTASES. STRONG, TO CEFE.
                                                                                                                                                                                                                      ij
                                                                                                                                                                      59.0%; Score 965.5; DB 1; Length 310; 61.2%; Pred. No. 9.4e-82; ive 37; Mismatches 80; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1901;
EMBL; 221687; CAA79803.1; -.
PIR; S40253; S40253.
InterPro; IPR005123; 20G-FeII Oxy.
Pam, PP03171; 20G-FeII_Oxy; I.
Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin C.
SEQUENCE 310 AA; 34364 MW; 9983EFIACIB416E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 AA
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                                                                                                                                                                                               Best Local Simitarity of Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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CEFF_STREL
CEFF_STREL
DT 01-NOV-
DT 01-NOV-
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63 EKAAVTIDVPTWRRGYSALEAESTAQVTRTGSYTDYSMSFSMGISGNVFPSPEFERVWTE 122
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                                                                                                                                                                                                                                                                                                           62 EKRAVISPVPIMRRGFICLESESTAQIINIGSYSDYSMCYSMGTADNLFPSGDFGRIWIQ 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cephalosporium acremonium (Acremonium chrysogenum).
Eukaryota, Fungi, Ascomycota, Pezizomycotina; Sordariomycetes;
Hypocreomycetidae, Hypocreales; Hypocreaceae; mitosporic Hypocreaceae;
                                                                                                                                                                                                                                              2 DITVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 KAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cephalosporin biosynthesis expandase/hydroxylase [Includes:
Deacetoxycephalosporin C synthetase (EC 1.14.20.1) (DACCS)
(Expandase); Deacetoxycephalosporin C hydroxylase (EC 1.14.11.-)
(Deacetylcephalosporin C synthetase) (DACS) (Beta-lactam
                                                                                                                                                               9
                                                                                                                   DB 1; Length 318;
InterPro; IPR005123; 20G-FeII Oxy. Pfam; PF03171; 20G-FeII Oxy; \overline{1}. Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin C.
                                                                  318 AA; 34584 MW; B17CC1CBC1E67178 CRC64;
                                                                              57.4%; Score 939.5; DB 1; Pred. No. 2.5e-79; "...hea 81;
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InterPro; IPR005123; 20G-FeII Oxy.
InterPro; IPR002057; Isopen N synth.
Pfam; PF03171; 20G-FeII_Oxy; I.
                                                                                                                                         Best Local Similarity 58.6
Matches 180; Conservative
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Q54243;
15-JUL-1999
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SEQUENCE
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                                                                                                                                                                                                61 AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWT 120
                                                                                                                                                                                                                      61 EEKRAVTLADRNARRGFSALEWESTAVVTETGKYSDYSTCYSMGIGGNLFPNRGFEDVWQ 120
                                                                                                                                                                                                                                             OYFDROYTASRAVAREVLRATGTEPDG-GVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLR 179
                                                                                                                                                                                                                                                          121 DYFDRMYGAAKDVARAVLNSVGAPLAGEDIDDFVECDPLLRLRYFPEVPEDRVAEEFPLR 180
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                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Isopenicillin N synthetase (EC 1.21.3.1) (Ipns) (Isopenicillin synthetase)
                                                                                                                             ï
                                                                                                   . Match 56.6%; Score 926.5; DB 1; Length 332; Local Similarity 56.7%; Pred. No. 4.2e-78; les 177; Conservative 43; Mismatches 91; Indels 1.
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MUTAGENESIS OF HISTIDINE AND ASPARTIC ACID RESIDUES.
MEDLINE=96229923; PubMed=8639682;
Borovok I., Landman O., Kreisberg-Zakarin R., Aharonowitz Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces jumonjinensis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
PROSITE; PS00185; IPNS_1; 1.
PROSITE; PS00186; IPNS_2; 1.
Antibiotic biosynthemis; Oxidoreductase; Iron; Vitamin (Multfunctional enthemis; Oxidoreductase; Iron; Vitamin (Multfunctional enthemis; IRON (BY SIMILARITY).
METAL 184 184 IRON (BY SIMILARITY).
METAL 244 244 IRON (BY SIMILARITY).
SEQUENCE 332 AA; 36479 MW; EOBDSCE68AA28B79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 AA
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 VPTIDISPLSGDDAKAKORVAO-EINKAARGSGFFYASNHGV---DVQLLODVVNEFHRN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 VPTFSL-----ABLOQGLHQDBFRRCLRDKGLFYLTDCGLTDTBLKSAKDLVIDFFBH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 -NLFPSGD----FGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCE----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLRFRYFPQVPEHRS-AEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 LIRYPYLEEYPPVKTGADGTKLSFEDHLDVSMITVLYQTEVQN----LQVETVDGWQDIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42; Gaps
PATHWAY: Biosynthesis of penicillin and cephalosporin. SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OXIDOREDUCTASES.
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15-JUL-1999 (Rel. 38, Last sequence update)
28-FBB-2003 (Rel. 41, Last amnotation update)
1sopenicillin N synthetase (EC 1.21.3.1) (IPNS) (Isopenicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 YRPDAVLVPCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFL 265
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MEDLINE=91197089; PubMed=1901702;
Garcia-Dominguea M., Liras P., Martin J.F.;
"Cloning and characterization of the isopenicillin N synthase control characterization of the isopenicillin N synthase streptomyces griseus NRRL 3851 and studies of expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSDEDFLVNCGTYMGHITHDYFPAPNHRV-----KFINAERLSLPFFL 284
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Bacteria, Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NGBI_TaxID=1911;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.9%; Score 179; DB 1; Length 32 24.9%; Pred. No. 5.1e-09; ive 45; Mismatches 130; Indels
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                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P05326; 1BK0.
InterPro; IPR002123; 20G-FeII Oxy.
InterPro; IPR002283; IPN_synth.
InterPro; IPR002057; Isopen N synth.
Pfam; PF03171; 20G-FeII Oxy; 1.
PRINTS; PR00682; IPNSYNTHASE.
PROSITE; PS00186; IPNS 1; 1.
PROSITE; PS00186; IPNS 1; 1.
Antibiotic biosynthee18; Oxidoreductase; Iron; Vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 268 IRON.
329 AA; 37305 MW; 9C8F1EB8FB8DFC6
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                                                                                                                                                                                                                                                                                                                                                         EMBL; M36687; AAA26772.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 24.9
hes 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
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                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its meeb by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SG---DFGRIW------TQYFDRQYTASRAVAREVLRATGTEPDGGVEA--- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RŚGTPMHEGNIWPDEKRHORFRPFCEGYYRDVFSLŚKVLMRGFALALG-KPEDFFDASLS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---FLDCEPLLRFRYFPQVPEHRSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LADTLSAVTLIHYPYLEDYPPVKTGPDGTKLSFEDHLDVSMITVLFQTEVQN----LQVE 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 VPIIDISPLSGGDADDKKRVAQEINKACRESGFFYASHHGI---DVQLLKDVVNEFHRTM 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 VGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEAEK-----RAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPTFSLAELQQGLHQD-----EFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 TADGWQDLPTSGENFLVNCGTYMGYLTNDYFPAPNHRV-----KFINAERLSLPFFL
                Antimicrob. Agents Chemother. 35:44-52(1991).

-I-FUNCTION: Removes, in the presence of oxygen, 4 hydrogen atoms from delter. -[alpha-aminoadipyl)-L-cysteinyl.-D-valine (ACV) to form the azeridinone and thiazolidine rings of isopenicillin.
-I-CATALYTIC ACTIVITY: N- ([58)-5-amino-5-carboxypentanoyl]-L-cysteinyl-D-valine + O(2) = isopenicillin N + 2 H(2)O.
-I-COFACTOR: Iron and ascorbate.
-I-PATHMAY: Bicosyntheeis of penicillin and cephalosporin.
-I-SIMILARIY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF OXIDOREDUCTASES.
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1-JUL-1989 (Rel. 11, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
18openicillin N synthetase (EC 1.21.3.1) (IPNS) (Isopenicillin N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60;
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larity 24.5%; Pred. No. 9.7e-09;
Conservative 39; Mismatches 126; Indels
complementation of the cephamycin pathway in Streptomyces
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RON (BY SIMILARITY).
RON (BY SIMILARITY).
0CD96C8F7CF5A7EB CRC64;
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InterPro; IPR002283; IPN synth.
InterPro; IPR002057; ISOpen N synth.
Pfam; PF03171; 20G-FeII Oxy; I.
PRINTS; PR00182; IPNSYNTHASE.
PROSITE; PS00185; IPNS 1; 1.
PROSITE; PS00186; IPNS 1; 1.
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329 AA; 37368 MW;
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HSSP; P05326; 1BK0.
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P10621;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEAEK-----RAVTSPVPTMRRGF----TGLESESTAQITNTGSYSDYSMCYSMGT---A 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 TDQEKHDLAIHAYNPDNPHVRNGYYKAVPGRKAVESFCYLNPDFGEDHPM-IAAGTPMHE 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46; Gaps
                                                                                                                                                                                                                                Leskiw B.K., Aharonowitz Y., Mevarech M., Wolfe S., Vining L.C., Westlake D.W.S., Jensen S.E.; "Cloning and nucleotide sequence determination of the isopenicillin synthetase gene from Streptomyces clavuligerus.";
                                                                                                                                                                                                                                                                                                                                                                                                   Gene 62:187-196 (1988).

-!- FUNCTION: Removes, in the presence of coxygen, 4 hydrogen atoms from delta-L-(alpha-aminoadipyl)-L-cysteinyl-D-valine (ACV) to form the azetidinone and thiazolidine rings of isopenicillin.
-!- CATALYTIC ACTIVITY: N | ([SS) -5-amino-5-carboxypentanoyl]-L-cysteinyl-D-valine + 0(2) = isopenicillin N + 2 H(2)0.
-!- COFACTOR: Iron and ascorbate.
-!- PATHWAY: Biosynthesis of penicillin and cephalosporin.
-!- SIMILARIY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF OXIDOREDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 329;
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IRON (BY SIMILARITY)
IRON (BY SIMILARITY)
Streptomycineae, Streptomycetaceae, Streptomycee.
NCBI_TaxID=1901;
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                                                                                                                SEQUENCE FROM N.A.
STRAIN=ATCC 27064 / DSM 738 / NRRL 3585;
MEDLINE=88212175; PubMed=3130293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276 PLARECGFDVSLDGETATFQDWI 298
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InterPro; IPR002283; IPN SYMEN.
InterPro; IPR0022057; Isopen N synth.
Pfam; PF03171; 2OG-FeII Oxy; I.
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329 AA; 36958 MW;
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PRINTS; PR00682; IPNSYNTHASE.
PROSITE; PS00185; IPNS 1; 1.
PROSITE; PS00186; IFNS 2; 1.
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                               -HYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPD 220
                                                                        -----PLKLGPDGEKLSFEHHQDVSLITVLYQTAIPN----LQVETAEGYLDIPVSDE 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 RCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEK-----RAVTSPVPTMRRGFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biosynthesis from Lysobacter lactamgenus YK90.";
Appl. Microbiol. Biotechnol. 4:589-596(1996).
-!-FUNCTION: Removes, in the present of oxygen, 4 hydrogen atoms from delta-L-(alpha-aminoadipyl)-L-cysteinyl-D-valine (ACV) to form the azetidinone and thiazolidine rings of isopenicillin.
-!- CATALYTIC ACTIVITY: N [(5S) 5-amino-5-carboxypentanoyl]-L-cysteinyl-D-valine + O(2) = isopenicillin N + 2 H(2)O.
-!- COFACTOR: Iron and ascorbate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kimura H., Izawa M., Sumino Y., "Molecular analysis of the gene cluster involved in cephalosporin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- PATHWAY: Biosynthesis of penicillin and cephalosporin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-UUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Isopenicillin N synthetase (EC 1.21.3.1) (IPNS) (Isopenicillin N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lysobacter lactamgenus.
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 326;
                                                                                                                                                              221 AVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFF 264
                                                                                                                                                                                                                            243 HFLVNCGTYMAHITNGYYPAPVHRV-----KYINAERLSIPFF 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEAM; PF03171; 20G-FeII Oxy; I.
PRINTS; PR00682; IPNSYNTHASE.
PROSITE; PS00188; IPNS_1; 1.
PROSITE; PS00186; IPNS_2; 1.
Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36564 MW; 25731F67173F8447 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; SSHUS; LERG.
HSSP, POSS26, 1BKO.
InterPro; IPR005123; 20G-FeII Oxy.
InterPro; IPR002283; IPN synth.
InterPro; IPR002057; ISOpen N synth.
                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=YK90;
MEDLINE=96287475; PubMed=8703429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X56660; CAA39983.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xanthomonadaceae; Lysobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                           170 HRSAEEQPLRMAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S54099; S54099.
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326 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OXIDOREDUCTASES
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es 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=39596;
                                                                                                                                                                                                                                                                                                                                                                                                  LYSLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthase).
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048739
                                                                                                                                                                                                                                                                                                                                    T 10
LYSLA
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IPNS_LY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 -----YMAVEGKKANESFCYLNPSFDADHATIKAGLPSHEVNIWPDEARHPGMRRFY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 TQYFDRQYTASRAVAREVLRATGTEPDGGVEAF-----LDCEPLLRFRYFPQVPE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 BAYFSDVFDVAAVILRGFALALGRE----ESFFERHFSMDDTLSAVSLIRYPFLENYP- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RACRGSGFFYAANHGV---DLAALQKFTTDWHMAMSAEEKWELAIRAYNPANPRNRNGY- 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 RCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEK-----RAVTSPVPTMRRGFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90174998; PubMed=2308852;
Shiffman D., Cohen G., Aharonowitz Y., von Dohren H., Kleinkauf H.,
Mevarech M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Nucleotide sequence of the isopenicillin N synthase gene (pcbC) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the Gram-negative Flavobacterium sp. SC 12,154.";

Nucleic Acids Res. 18:660-660(1990).

-! FUNCTION: Removes, in the presence of oxygen, 4 hydrogen atoms from deltea-L-(alpha-aminoadippl)-L-cysteinyl-D-valine (ACV) to form the azetidinone and thiazolidine rings of isopenicillin.

-!- CATALYTIC ACTIVITY: N - ([55)-5-amino-5-carboxypentanoyl]-L-cysteinyl-D-valine + 0(2) = isopenicillin N + 2 H(2)0.

-!- COFACTOR: Iron and ascorbate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: BIOSYNTHEBIS OF PENICILLIN and Cephalosporin. SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF OXIDOREDUCTASES.
                                                                                                                                                                                                                         01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Isopenicillin N synthetase (EC 1.21.3.1) (IPNS) (Isopenicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Flavobacterium sp. (strain SC 12,154).
Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF03171; 20G-Fell C., Pfam; PF03171; 20G-Fell C., Prints; PR00682; IPRSYTHASE. PROSITE; PS00185; IPNS 1; 1.
PROSITE; PS00186; IPNS 2; 1.
Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin (209 209 IRON (BY SIMILARITY).
TRON (BY SIMILARITY).
TRON (BY SIMILARITY).
TRON (BY SIMILARITY).
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1.9e-07;
                                                                                                                                                                  326 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.9%; Score 162;
22.9%; Pred. No. 1
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294 PFVPE-GASEEVRNEALSYGDYL 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR005123; 20G-FeII Oxy.
InterPro; IPR002283; IPN synth.
InterPro; IPR002057; Isopen N synth.
Pfam; PF03171; 20G-FeII Oxy; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flavobacteriaceae; Flavobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X17355; CAA35233.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.9%;
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                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=241;
                                                                                                                                                           IPNS FLASS
P16020;
                                                                                                                                                                                                                                                                                                                                                                   synthase).
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                                                                                                                               IPNS FLASS
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                                                                                                                                                     170 HRSABEQPLRMAP-----HYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPD 220
                                                                                                                                                                            194 -----PLKLGPDGEKLSFEHHQDVSLITVLYQTAIPN----LQVETAEGYLDIPVSDE 242
GLESESTAQITNTGSYSDYSMCYSMGTAD------NLFPS----GDFGRIW 119
                                    -----YMAVEGKKANESFCYLNPSFDADHATIKAGLPSHEVNIWPDEARHPGMRRFY 139
                                                                                                               140 EAYFSDVFDVAAVILRGFAIALGRE----ESFFERHFSMDDTLSAVSLIRYPFLENYP- 193
                                                                          TQYFDRQYTASRAVAREVLRATGTEPDGGVEAF-----LDCEPLLRFRYFPQVPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nidulans.";
J. Bacteriol. 170:3817-3826(1988)

-!-FUNCTION: Removes, in the presence of oxygen, 4 hydrogen atoms from delta-L-(alpha-aminoalpiyl)-L-cysteinyl-D-valine (ACV) to form the azetidinone and thiazolidine rings of isopenicillin.
-!- CATALYTIC ACTYUTY: N-[(58)-5-amino-5-carboxypentanoyl]-L-cysteinyl-D-valine + O(2) = isopenicillin N + 2 H(2)O.
-!- COPACTOR: Iron and ascorbate.
-!- PATHWAY: Biosynthesis of penicillin and cephalosporin.
-!- SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=88314868; PubMed=3045077;
Weigel B.J., Burgett S.G., Chen V.J., Skatrud P.L., Frolik C.A.
Queener S.W., Ingolia T.D.,
"Cloning and expression in Escherichia coli of isopenicillin N
synthetase genes from Streptomyces lipmanii and Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Isopenicillin N synthetase (EC 1.21.3.1) (IPNS) (Isopenicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 HFLVNCGTYMAHITNGYYPAPVHRV-----KYINAERLSIPFF 280
                                                                                                                                                                                                                                  221 AVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFF 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D55385664EA2CA26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces lipmanii (Streptomyces alboniger)
                                                                                                                                                                                                                                                                                                                                                                      333 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR05123; 20G-FeII Oxy.
InterPro; IPR002283; IPN_synth.
InterPro; IPR002057; ISopen_N synth.
Pfam; PF01317; 20G-FeII Oxy; I.
PRINTS; PR00682; IPNSYNTHASE.
PROSITE; PS00185; IPNS 1; 1.
PROSITE; PS00186; IPNS 1; 1.
                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38082 MW;
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                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OXIDOREDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=132472;
                                                                                                                                                                                                                                                                                                                                                                    IPNS STRLP
P12438;
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SEQUENCE
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                                         13;
                                                                                                                                                                  109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286
                                                                                                                                                                                                         66 MTDQEKHDLAIHAYNENNSHVRNGY-----YMARPGRKTVESWCYLNPSFGEDHPM 116
                                                                                                                                                                                                                                                     110 FPSG-----EPDGTIWTQYFDRQYTASRA-VAREVLRATGT-----EPDG 147
                                                                                                                                                                                                                                                                                             117 IXAGTPMHEVNVWPDEERHPDFRSFGEOYYREVFRLSKVLLLRGFALALGKPEEFFENEV 176
                                                                                                                                                                                                                                                                                                                                      148 GVEAFLDCEPL-LRFRYFPQVPE---HRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVS 203
                                                                                                                                                                                                                                                                                                                                                                                                                          204 LQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVF 263
                                                                                                                          65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. Old Glory Blue; TISSUE=Petal;
MEDLINE=94108485; PubMed=7904213;
MEDLINE=94108485; PubMed=7904213;
MEDLINE=94108485; PubMed=7904213;
MEDLINE=94108485; PubMed=7904213;
MICIONI and expression of flavonol synthase from Petunia hybrida.";
Plant J. 4:1003-1010(1993).
-! FUNCTION: CATALYZES THE FORMATION OF FLAVONOLS FROM
DIHYDROPLAVONOLS. IT CAN ACT ON DIHYDROKAEMPFEROL TO PRODUCE
KAEMPFEROL, ON DIHYDROQUERCETIN TO PRODUCE QUERCITIN AND ON
DIHYDROMYRICETIN TO PRODUCE MYRICETIN.
-! CORCIOR: IRON AND ASCORBATE.
-! PATHWAY: PART OF THE BLOSYWTHEIT. PATHWAY FOR FLAVONOLS WHICH ARE
FLAVONOLDS. FLAVONOLS ARE IMPORTANT CO-PIGMENTS IN FLOWER OR FRUIT
COLOR AND ARE ALSO ESSENTIAL FOR POLLEN TUBE GROWTH.
                                                                                                         10 VPIIDISPL-FGTDPDAKAHVARQINEACRGSGFFYASHHGI---DVRRLQDVVNEFHRT
                                                                                                                                                                  58 GSEAEK----RAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCY---SMGTADNL
                                                                                                                                                                                                                                                                                                                                                              5 VPTFSLAELQQGLHQD-----EFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 LÓVETVDGWOSLPTSGENFLINCGTYLGYLTNDYFPAPNHRV-----KYVNABŘLSLPP
                                         64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Cytoplasmic.
DEVELOPMENTAL STAGE: EXPRESSED AT HIGHEST LEVEL DURING THE FIRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamids; Solanales; Solanaceae; Petunia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF OXIDOREDUCTASES.
  Length 333;
                                         37; Mismatches 131; Indels
8.7%; Score 143; DB 1;
23.2%; Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
16-077-2001 (Rel. 40, Last annotation updat.
Flavonol synthase (EC 1.14.11.-) (FLS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STAGE OF FLOWER DEVELOPMENT.
Query Match
Best Local Similarity 23.2%
Matches 70; Conservative
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                                        PIR; S15284; S15284.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 TAQITUTGSYSDYSMCYSMGTADNLF-----PSGDFGRIW-------TQYFDRQYT 128
                                                                                                                                                                                                           129 ASRAVAREVLRATGTEPDGGVEAFLDCE--PLLRFRYFPQVPEHRSAEEQPLRMAPHYDL 186
                                                                                                                                                                                                                              182 VVDRIFKSLSLGLGLEGHEMIEAAGGDEIVYLKINYYPPCPR----PDLALGVVAHTDM 237
                                                                                                                                                                                                                                                  SMVTLIQQIPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVA 246
                                                                                                                                                                                                                                                             137 EGK------KGWVDHLFHKIWPPSAVNYRYWPKNPPSYREANEEYGKRMRE 181
                                                                                                                                84
                                                                                                                               RDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVT-SPVPTMRRGF-TGLESES
                                                            ပ
                                                                                                           Gaps
                  InterPro; IPR005123; 20G-FeII Oxy.
InterPro; IPR002283; IPN synth.
Pfam; PF03171; 20G-FeII Oxy; 1.
PRINTS; PR00682; IPNSYNTHARS.
PRINTS; PR00682; IPNSYNTHARS.
SEQUENCE 348 AA; 39427 MW; B39EIE438IDE6379 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Isopenicillin N synthetase (EC 1.21.3.1) (IRNS) (Isopenicillin)
                                                                                                           48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
                                                                                      8.6%; Score 140; DB 1; Length 348; 22.3%; Pred. No. 2.2e-05; iive 43; Mismatches 114; Indels 4
                                                                                                                                                                                                                                                                                                                                                            328 AA
                                                                                                                                                                                                                                                                                         247 APRRDQIAGSSRTSSVFFLRPNAD 270
                                                                                                                                                                                                                                                                                                            294 VNK-----DKTRMSWPVFLEPPSE 312
                                                                                                                                                                                                                                                                                                                                                           PRT;
 Z22543; CAA80264.1; -.
                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Nocardia lactamdurans
           PIR; S33510; S33510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OXIDOREDUCTASES
                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                           IPNS NOCLA
                                                                                                                                                                                                                                                                                                                                                                                                                       synthase).
                                                                                                                               27
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                                                                                         Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 SPQEKYDLAIHAYNKONSHVRNGYYMAIEGKKAVE-----SPCYLNPSFSEDHPE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 -SMGT---ADNLFPSGD----FGRIWTQYFDRQYTASRAVAREVLRATGT-----EPDGG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 VEAFLDCEPLLRFRYFPQVPEHRSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 EADTLSSVSLIRYPYLEDYPPVKTGPDGEKLSFEDHFDVSMITVLYQTQVQN----LQVE 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 IKAGTPMHEVNSWPDEEKHPSFRPFCEEYYWTMHRLSKVLMRGFALALGKDERFFEPELK 174
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"Flavonol synthase gene expression during citrus fruit development.";
Physiol. Plantarum 114:251-258 (2002).
-!- FUNCTION: CATALYZES THE FORMATION OF FLAVONOLS FROM
DIHYDROPLAVONOLS. IT CAN ACT ON DIHYDROCAEMPERED. TO PRODUCE
KAEMPERED. ON DIHYDROQUERCETIN TO PRODUCE OUERCITIN AND ON
DIHYDROMYRICETIN TO PRODUCE MYRICETIN (BY SIMILARITY).
-!- COFACTOR: IRON AND ASCORBATE (BY SIMILARITY).
-!- PATHWAY: PART OF THE BLOSYMHETIC PATHWAY: POR FLAVONOLDS WHICH ARE
FLAVONOLDS. FLAVONOLS ARE IMPORTANT CO-PICHENTS IN FLOWER OR FRUIT
COLOR AND ARE ALSO ESSENTIAL FOR POLLEN TUBE GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 VGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFF 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 TVDGWRDLPTSDTDFLVNAGTYLGHLTNDYFPSPLHRV-----KFVNAERLSLPFF 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 VPTFSLAELQQGLHQD-----EFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 SEAEK----RAVTSPVPTMRRG-FTGLESESTAQITNTGSYSDYSMCY-----
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 328;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Mismatches 129; Indels
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METAL 216 26 IRON (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 AA; 37466 MW; FODE8B0727AC3855 CRC64;
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28-FEB-2003 (Rel. 41, Last annotation update)
Flavonol synthase (EC 1.14.11.-) (FLS) (CitFLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.4%; Score 138; DB 1; 22.6%; Pred. No. 3.1e-05;
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                                                                                                                                                                      HSSP, P05326; IBRO.
InterPro; IPR005123; 20G-FeII Oxy.
InterPro; IPR005123; IPN_synth.
InterPro; IPR002037; ISOPen N synth.
Pfam; PF03171; 20G-FeII Oxy.
PRINTS; PR00682; IPNSYNTHASE.
PROSITE; PS00186; IPNS 1; 1.
PROSITE; PS00186; IPNS_2; FALSE_NEG.
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16-OCT-2001 (Rel. 40, Last seq
28-FEB-2003 (Rel. 41, Last ann
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PubMed=11903972;
                                                                                                     EMBL; X57310; CAA40562.1; -
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                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 NYRFWPKNPPSYRAVNEEYAKYMREVVDKLFTYLSLGLGVEGGVLKEAAGGDDIEYMLKI 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 NYYPPCPR----PDLALGVVAHTDLSALTVL----VPNEVPGLQVFKDDRWIDAKYIPNA 255
                                                                                                                                                                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --OYFDRQYTASRAVAREVLR------ATGTEPDGGV--EAF--LDCEPLLRF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 IPTIDLDDPVQDRLVRSIAEASREWGIFQVTNHGIPSDLICKLQAVGKEFFELPQE-EKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVTSPVPTMRRGFTGLESESTAQ1TNTGSYSDYSMCYSMGTADNLFPSGDFGRIWT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RYPPOVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDA
                                                                                                                                                                                                                                                                                                                                                                                                                    5 VPTPSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKR
             TISSUE SPECIFICITY: In the juice sacs/segment epidermis (edible part) at the early developmental stage.
                                                                                                                                                                                                                                                                InterProj IPR09123; 20G-FeII Oxy.
Pfam; PF03171; 20G-FeII Oxy; I.
Flavonoid biosynthesis; Oxidoreductase; Dioxygenase; Iron; Vitamin SEQUENCE 335 AA; 37899 MW; 157EIAFA4C47564B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from Streptomyces cattleya.";
Acta Microbiol. Sin. 36:87-92(1996).
Alta Microbiol. Sin. 36:87-92(1996).
FuncTION: Removes, in the presence of oxygen, 4 hydrogen atoms from delta-L-(alpha-aminoadipyl)-L-cysteinyl-D-valine (ACV) to form the azetidinone and thiazolidine rings of isopenicillin.
-!- CATALYTIC ACTIVITY: N-[(SS)-5-amino-5-carboxypentanoyl]-L-cysteinyl-D-valine + 0(2) = isopenicillin N + 2 H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang Y., Li R.; "Cloning and sequencing the isopenicillin N synthetase (IPNS) gene
                                                                maturation.
SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                    55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FBB-21003 (Rel. 41, Last annotation update)
18openicillin N synthetase (EC 1.21.3.1) (Isopenicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 VLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNAD 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVIHIGDQIEILSNGKYKAVLHRTTVNK-----DKTRMSWPVFLEPPAD 299
                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                              DEVELOPMENTAL STAGE: Increases in the peel during fruit
                                                                                                                                                                                                                                                                                                                                                                                   124; Indels
 SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomycineae, Streptomycetaceae, Streptomyces
NCBI_TaxID=29303;
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21.8%; Pred. No. 3.6e
Live 47; Mismatches
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                                                                                                                                                                                                                                                      EMBL; AB011796; BAA36554.1; -.
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 21.8 Matches 63; Conservative
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                                                                                            OXIDOREDUCTASES
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053932;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 EVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLR 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 EAFLDCEPLLRFRYFPQVPE---HRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 EDTLSAVSMIRYPYLDPYPEAAIKTGPDGTRLSFEDHLDVSMITVLSKTEVQN----LQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 ETVDGWQSLPTSGENFLINCGTYLGYLTNDYFPAPNHRV-----KYVNAERLSLPFFLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 VPTFSLAELQQGLHQDEFR-----RCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 GSEAEKRAVTSPVPTMRRGFTGLESESTAQ----ITNTGSYSDYSMCY---SMGTADNLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 VPIIDISPQLFGTDPTPRRTSRGRSTRPARGSGFFYASHHGIDVRRLQTWSN-----
                       PATHWAY: Biosynthesis of penicillin and cephalosporin. SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36576 MW; BCC0CFFCF7C07AF1 CRC64;
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IRON (BY SIMILARITY)
IRON (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR005123; 2OG-FeII Oxy.
InterPro; IPR002283; IPW SYME.
InterPro; IPR002057; ISOPen N symth.
Pfam; PF03171; ZOG-FeII_OXy; I.
COFACTOR: Iron and ascorbate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRODG82; IPNSYNTHASE.
PROSITE; PSO0185; IPNS_1; 1.
PROSITE; PSO0186; IPNS_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    llarity 23.1%;
Conservative 3
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269
321 AA;
                                                                                         OXIDOREDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
es 73; Conserv
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Job time : 18 secs
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SEQUENCE
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Title: Perfect score:

Sequence:

protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Q9fab9 streptomyce
Q91c25 streptomyce
Q81c25 streptomyce
Q81c35 arabidopsis
Q80850 arabidopsis
Q80850 arabidopsis
Q80850 arabidopsis
Q9fab7 cryza sativ
Q39112 arabidopsis
Q9fab7 oryza sativ
Q91k4 arabidopsis
Q9fsk9 streptomyce
Q91k4 arabidopsis
Q9fsk9 streptomyce
Q91k4 arabidopsis
Q861g1 yersinia pe
Q801g1 yersinia pe
Q801g2 nierembergi
Q80029 yersinia pe
Q801g2 nierembergi
Q80620 oryza sativ
Q04280 phasseolus v
Q91k4 oryza sativ
Q04282 phasseolus v
Q91k4 oryza sativ
Q04282 phasseolus v
Q91k4 oryza sativ
Q04282 phasseolus v
Q91k4 oryza sativ
Q04003 malus domes
Q9fs09 malus domes
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Deacetoxycephalosporin C synthase.
Streptomyces jumonjinensis.
Bacteria; Actinobacteria; Actinobacteria; Actinomycetales; Streptomycineae; Streptomyces.
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 83.6%; Score 1369; DB 2; Length 311; Best Local Similarity 81.4%; Pred. No. 1.4e-119; Matches 253; Conservative 28; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SIM T.S., Sim J.;
Sim T.S., Sim J.;
"Cloning and purification of Streptomyces jumonjinensis deacetcxycephalosporin C synthase.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF317908, AAL03460.1, -.
InterPero; IPR005123; 20G-FeII_0xy.
InterPero; IPR002123; 20G-FeII_0xy.
InterPero; IPR002127; Isopen_N.gynth.
Pfam; PP03117; 20G-FeII_0xy;
I. 20G-FEII_0xy;
II. 20G-FEII_0xy;
III. 20G-FEII_0xy;
III.
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Q39112
Q9F5K9
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Q8ZG11
Q8ZG11
Q8D029
Q9BN75
Q8LP22
Q8LP22
Q8LP20
Q8SBB7
Q8SBB7
Q8SBB7
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Q9SBB7
Q9FS09
Q9FS09
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Q8SB89
Q9C955
O80850
Q9FAB7
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Q9LIF4
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            PRELIMINARY;
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            293FD4
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Q954t5 cephalospor
Q48741 lysobacter
Q987v6 rhizobium l
Q987v6 rhizobium l
Q96xc2 dresptomyce
Q96xc2 dresptomyce
Q95xc3 dresptomyce
Q95xc0 streptomyce
Q95xc0 streptomyce
Q95xc1 streptomyce
Q95xc3 streptomyce
Q95xc3 streptomyce
Q95xc3 streptomyce
Q95xc3 streptomyce
Q95xc3 streptomyce
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                                                                                                                                                                               February 3, 2004, 17:34:58; Search time 41 Seconds (without alignments) 1957.423 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                   1 MDTTVPTFSLAELQQGLHQD......ATFQDWIGGNYVNIRRTSKA 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             830525
                                    GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   - protein search, using sw model
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048740
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099VCZ2
09
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fung1:*
sp_human:*
sp_mammal:*
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sp_organelle:*
sp_phage:*
sp_phage:*
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seq length: 200000000
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1637
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                                                 APHYDLSMYTVIQQTPCPNGFVSLQAEIGGAFVDLPAKPDAVLVFCGAIATLYTGGQVKA 240
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          240
                                                                              PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
                                                                                        EKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQ 121
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                                       APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA
                                                                                                                                                                                                                                                                                                                STRAIN=YR90;
MEDLINE=96287475; PubMed=8703429;
Kimura H., Izawa M., Sumino Y.;
Kimura H., Izawa M., Sumino Y.;
"Molecular analysis of the gene cluster involved in cephalosporin biosynythesis from Lysobacter lactamgenus YK90.";
pppl. Microbiol. Biotechnol. 44:589-596(1996).
EMBL; X56660; CAA39984.1; --
InterPro; IRN05123; 20G-FeII_Oxy.
Pfam; PF03171; 20G-FeII_Oxy; 1.
                                                                                                                                                                                                                                                    Lysobacter lactamgenus.
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
Xanthomonadaceae, Lysobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                  319 AA; 35559 MW; 51040CD201B7C272 CRC64;
                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Best Local Similarity 58.09
Matches 177; Conservative
                                                                                                                                 NYVNIRRISKA 311
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01-NOV-1996 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 APRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 APKHRVKSPGRDQRVGSSRTSSVFILRRKPDFSFNVQQSREWGFNVRIPSERTTFREWLG 300
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                                                                                                                                                                                                                                                                                                                       Jekosch K., Nosek J., Kueck U.;
"Analysis of cefEF gene expression in two cephalosporin C producing strains of Acremonium chrysogenum.";
Submitted (JUL-2000) to LHE EMBL/GenBank/DDBJ databases.
EMBL, AJ404737; CAB96750.1;
InterPro; IPR0020123; 20G-FeII_Oxy.
InterPro; IPR0020127; Isopen. N synth.
PROSITE; PS00185; IPNS 1; 1.
PROSITE; PS00186; IPNS 1; 1.
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                                                                                                                                                                                   Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Hypocreales, Hypocreaceae, mitosporic Hypocreaceae, Acremonium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 56.0%; Score 917.5; DB 3; Length 332; Best Local Similarity 56.4%; Pred. No. 2.4e-77; Matches 176; Conservative 43; Mismatches 92; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E3DEECE5E9C28B79 CRC64;
                                                  01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Deacetylcephalosporin C synthetase/hydroxylase.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Deacetylcephalosporin C synthetase.
                                                                                                                                                                Cephalosporium acremonium (Acremonium chrysogenum)
    332
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    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 AA; 36538 MW;
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NCBI_TaxID=39596;
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    PRELIMINARY;
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SEQUENCE FROM N.A.
STRAIN=YK90;
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Q9ANU0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 NRMAPHYDLSIVSLILQTPCPNGFVSLQVEIDGRFVSVPPRPGCVVVFCGSIAPLVSDGK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 GSEAEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 IWTOYFDROYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQP 177
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                                                                                                                                                                                                                                                                                                                                                                                     2 DTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKD----LVIDFFEH 57
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Kimura H., Izawa M., Sumino Y.; Molecular analysis of the gene cluster involved in cephalosporin biosynythesis from Lypobacter lactamgenus YK90."; Appl. Microbiol. Biotechnol. 44:589-596(1996). "Biotechnol. Hiotechnol. 14:589-596(1996). "InterPro: IPRO5123; ZOG-Pell. Oxy. Pfam; PF03171; ZOG-Pell.Oxy; I.
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Phyllobacteriaceae; Mesorhizobium.
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SEQUENCE 366 AA; 40188 MW; 67EDD760AFFDC0C9 CRC64;
                                                                                                                                                                                                                     313 AA; 34418 MW; 4C341A6FFE771CD6 CRC64;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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InterPro; IPR005123; 20G-Fe1I Oxy.
InterPro; IPR002283; IPN synth.
Pfam; PF03171; 20G-Fe1I Oxy; 1.
PRINTS; PR00682; IPNSYNTHASE.
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299 CGANYMEMHVTT 310
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                                                                                                                                                                                                                     SEQUENCE
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10.3%; Score 168; DB 16; Length 366;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                    249 SWYDVDPIPGTLVVNIGELLELASNGYLRATVHRVVTPP----AGVERISVPFFFSARLD 304
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                                                                                                                                                                                                                                                                                                                                                      116 GRIWTQ-YFDRQYTAS------RAVAREVLRATGTEPDGGVEAFLDCEPLL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 ----YSSEPNHRMKIVRYPGRDTTGGDQGVGAHKDGGFLTLLLQ----DDNKGLQVDYDG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 AFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNAD 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 SEAEK-----RAVISPVPTMRRG-FTGLESESTAQITNTGSYSDYSMCY---SMGTADNL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---FGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEA-- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=JCM 4910; Sim T.S., Yo C.Y., Wong B.; Sim T.S., Yo C.Y., Wong B.; "Genome walking and PCR-based cloning of isopenicillin N synthase gene
                                                                                                 1 MDTTVPTFSLAELQQGLHQ-----DEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 RFRYFPQVPEHR-SAEEQPLR-----MAPHYDLSMVTLIQQTPCANGFVSLQAEVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 VPTPSLABL-----QQGLH-QDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 VPTIDISPLFGDDPDAKTHVAQQINKACRGSGFFYASHHGI----DVQQLQDVVNEFHGTM
                                                                                                                                                      28 MPRIVPVLDLSRLEQGASERRTFLADLRSASRDIGFFYLAGHGISWAEISBVLTASRQFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.8%; Score 161; DB 2; Length 329;
23.4%; Pred. No. 1.2e-06;
tive 42; Mismatches 125; Indels 62; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=68197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 FT----FSVPLARECGFDVSLDGETATFQDWIGGNYVNIRRTS 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 ATIPLIGLSEELAAQARGPAS-DPDNPLFRD-VGTNVLKSRLRS 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from Streptomyces fimbriatus.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF320779; AAK11177.1;
InterPro; IPR05123; 20G-FeII Oxy.
InterPro; IPR00253; IPUS synth.
InterPro; IPR002057; Isopen W synth.
PF03171; 20G-FeII Oxy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0662; IPNSYNTHASE.
PROSTITE; PS00185; IPNS 1; 1.
PROSTITE; PS00186; IPNS 2; 1.
SEQUENCE 329 AA; 37232 MW; 4BC3CA090CC556A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                 41; Mismatches 158;
      Pred. No. 3.2e-07
24.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 23.44
Matches 70; Conservative
   Best Local Similarity 24.7
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sopenicillin N synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces fimbriatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 FPSGD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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SUCENCE FROM N.A.

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RAM AMADIANE STROWN N.A.

RAM AMADIANE STROWN N.A.

RAM AMADIANE ST. S. HOLT R.A., FOANDS C.A., GOCCATHE J.D.,

RAM AMADIANE ST. SCHERTS S.E., LIPPW. HOSKINS R.A., GGALLE R.F.,

RAM AMADIANE ST. S. RICHARGE S., ABABDHURDET M., HENDERSON S.N.,

SULFON G.G., WORTHAN J. S. T. RICHARGE S., ABABDHURDET M., HENDERSON S.N.,

BANDIAN S.C., ROGGER Y.-H.C., BARCH S.G., CHAMDE M., PERIFECT B.D.,

RAM R.H., DOYLE C., BARCH S.G., CHAMDE M., PERIFECT B.D.,

RAM AND R.H., BASH A., AN H.-J., ANGREWS PERMINCOH C., BAIGHAIN D.,

RAM BAILL W.R., BASH A., BASH M.-J., BANDRASH J.D., BOLD SHAKOW S.,

RAM BAILW R.M., CAWLES B. DANIER M., CARGER A., CHANDRA I.,

RAM CHETY J.M., CAWLES S., DANIER M., DENCE A., CHANDRA I.,

RAM CHETY J.M., CAWLES S., DANIER M., DENCE A., DENCE A., CHANDRA I.,

RAM CHETY J.M., CAWLES S., DANIER M., DEAD S., DINKW S., DINK S.,

RAM CHETY J.M., CAWLES S., DANIER M., DEAD S., DINKW S., DINK S.,

RAM CHETY J.M., CAWLES S., DANIER M., DEAD S., DINK N., GADYLELIA M. A., HOWLE S., S., DINK W., S.,

RAM CHATY J.M., HARVOY D., HEALMAN T.J., HETMARCH S., FLAIS M.,

RAM HATIS N.L., HARVOY D., HEALMAN T.J., HETMARCH S., ROLL M., S.,

RAM HATIS N.L., HARVOY D., HEALMAN T.J., HETMARCH S., ROLL M., NORL M.,

RAM HATIS N.L., HARVOY D., MEALMAN T.J., MEALMAN S., HOUCK J.,

RAM HATIS N.L., MARTON D., MONDARY C., MORTIS J., MORDHERE S., MONDHERE S.,

RAM LIN S., MORIER S., MONDARY C., MORTIS J., MORDHERE S., MOLD S.,

RAM MOUNT S.M., WOY M., WINDON Y., MURDY L., MURDY D.M., NALSON D.L.,

RAM BENEVER C., SIGHER S., PROMINGER R., PORTIS R., WAND S., WAND S.,

RAM BENEVER S., REALDEND R.A., MINDON S., SCHEELE F., SHAN H.,

RAM SEAL S., SPREADLING N., SAURDER E., SARLH T.,

RAM SEAL S., SPREADLING N., SAURDER E., SARLH T.,

RAM SEAL S., SPREADLING S., SAURDER E., SARLH T.,

RAM SEAL S., SAURDER S., WOLTER E., WORTHER E., SAURD D.L.,

RAM SEAL S., SAURD S., SAURDER E., SAURD S., SAULD S.,

RAM SEAL TECCOT C., TURTER R., WELLE E., SAURD D.L.,

RAM SEAL S., SAURDER S., ROGGER T., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A carlson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Feritaer S., Frise B., Galle R.F., Garg N.S., George R.A.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
A phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Sequencing of Drosophila melanogaster genome.",
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE PROM N.A.
Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
                                                                                                                               Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Haxapoda; Insecta, Pterygota,
Neoptera, Endopterygota, Diptera; Brachycera, Muscomorpha;
Ephydroidea, Drosophilidae, Drosophila.
                           Last sequence update)
Last annotation update)
  Created)
(TrEMBLrel.
                           (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                NCBI_TaxID=7227;
                                                                                 CG5346 protein.
  176 PEDDILSAVSLIRYPHLKAYPPVKTGPDGTKLSFEDHLDVSVITVLFQTEVQN----LQV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 GP----TGLESESTAQITNTGSYSDYSMCYSMGT---ADNLFPS----GDFGRIWTQYFD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 GYYMAVKGKKAVESWCYLNPSFSEDHPMIRS-GTPMHEVNIWPDEKRHARFRPFCEQYYR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 ROYTASRAVAREVLRATGTEPDGGVEA-----FLDCEPLLRFRYFPQVPEHRSAEE-QP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 LRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQ 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 LSFEDHLDVSMITVLFQTEVQN----LQVETVDGWQDLPTSGENFLVNCGTYMGYLTNDY 247
  17 IRSGTPMHEVNIWPDEKRHERFRPFCEQYYRDMFQLSKTLMRGFALALG-KPEDFFDANL 175
                                                        152 ----FLDCEPLLRFRYFPQVPEHRSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 BINKACRGSGFFYASHHGI---DVQLLQDVVNEFHRTWTDEEKYDLAINAYNKDNPHVRN 73
                                                                                                                                                             207 EVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFL 265
                                                                                                                                                                                                             232 ETVNGWODLPTSGDDFLVNCGTYMGYLTNDYFPAPNHRV-----KFINAERLSLPFFL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palaniappan N., Seki T.;
"Phylogenetic relationship between the Isopenicillin N synthase (IPNS) and 16S rDNA genes.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB046951; BAB13299.1; -.
HSSP; P05326; 1BK0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 BFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEK-----RAVTSPVPTMRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces panayensis.
Bacteria, Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           th 9.7%; Score 159; DB 2; Length 262; Similarity 25.4%; Pred. No. 1.4e-06; 3; Conservative 38; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 AA; 30074 MW; D9A5D0BAB942D776 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UJUN-2002 (TrEMBLrel. 21, Last annotation update)
18openiallin N synthase (IPNS) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR005123; 20G-FeII Oxy.
InterPro; IPR002283; IPN synth.
InterPro; IPR002057; Isopen N synth.
Pfam; PF03171; 20G-FeII Oxy; I.
PRINTS; PR00682; IPNSYNTHASE.
PROSITE; PS00186; IPNS_1; I.
                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 VKAPRHHV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 FPAPNHRV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-JCM 5042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9VCZ2
Q9VCZ2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                               Q9FAC2
Q9FAC2;
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RESULT 8
Q9VCZ2
ID Q9VC
AC Q9VC

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105 123

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238 NEVDGPNGQLFEHKLGNGAVIQCPPHVDYGTFTLLSQD--SEGGLEVRLPGSEKWNRVGH 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 --ADNL----FPSGDFGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFL----- 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 LNAQNLPEEPLPG-----FADHISTLATDFKALASFILQALAVSLDIPHTFFLEKHSHM 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 LSGDHDNMSSLRMLYYPPIVDDEPGQNDVIKGRCQYSYQRCLSNQPDFRPEHNPRDEDDL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----RMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Palaniappan N., Seki T.;
Palaniappan N., Seki T.;
Phylogenetic relationship between the Isopenicillin N synthase (IPNS) and 16S rDNA genes.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB045853; BAB13301.1; -.
HSSP; P05326; IBKO.
InterPro; IPR002513; 20G-FeII Oxy.
InterPro; IPR002057; Isopen_N synth.
InterPro; IPR002057; Isopen_N synth.
PROSITE; PR00181; IPNS/NTHASE.
PROSITE; PS00186; IPNS_1; 1.
                                                                                                                                                                                                                                                                                                        3 TTVPTFSLAELOQGLHQ------DEFRRCLRDKGLFYLTDCGLTDTELKSAKDLV
                                                                                                                                                                                                                                                                                                                                                                                  52 IDPFEHGSEAEKRAVTSPVPTMRRGFTGLESESTAQITN-----TGSYSDYSMCYSMGT
                                                                                                                                                                                                                                                                                                                                                                                                                                     -----VNLP-PDIROHYIRADGDKHGYVSRGQQQRFDGKSPELRHAFNIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---PEHRSAEEQPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 EFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEK-----RAVTSPVPTMRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 LPGSILVNCGEILNIWTQGRYPALQHRVIIPEQETIRARGRHSIAFFCHPDNITTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 RPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFS
                                                                                                                                                                 Length 403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indele
EMBL; AY102699; AAM27528.1; -.
Flydase; FBgn0038981; CG5346.
Interpro; IPR005123; 2OG-FeII Oxy.
Pfam; PF03171; 2OG-FeII Oxy; 1.
SEQUENCE 403 AA; 45461 MW; DEZCBC0FD443A07C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 AA; 30122 MW; 3AFED20F3DB41E69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Isopenicillin N synthase (IPNS) (Fragment).
                                                                                                                                                                                       Best Local Similarity 20.2%; Pred. No. 4.3e-06; Matches 72; Conservative 51; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI TaxID=132471;
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                                                                                                                                                                 DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 AA
                                                                                                                                                                 9.6%; Score 156.5;
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01-WAR-2001 (TrEMBLrel. 16, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 ----DCEPLLRFRYFPQV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                        76 DDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 IDFFEHGSEAEKRAVTSPVPTMRRGFTGLESESTAQITN-----TGSYSDYSMCYSMGT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ADNL----FPSGDFGRIWTQYFDRQYTASRAVAREVLRATGTEFDGGVEAFL---- 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 LSGDHÖNMSSLRMLYYPPIVDDEPGQNDVIKGRCQYSYQRCLSNQPDFRPEHNPRDEDDL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----RMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 LPGSILVNCGEILNIWTQGRYPALQHRVIIPEQETIRARGRHSIAFFCHPDNITTIS 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 TTVPTFSLAELQQGLHQ------DEFRRCLRDKGLFYLTDCGLTDTELKSAKDLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 RPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFS
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Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Calamp M., Drysdale R., Emert D., Frise B., de Grey A., Harris N., Krommiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak P., Whitfield E., Sabburner M., Galbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                       Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.6%; Score 156.5; DB 5; Length 403;
20.2%; Pred. No. 4.3e-06;
Live 51; Mismatches 127; Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroida, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AE003739; AAF56013.2; -. FlyBase; FBGN0038981; CG5346. InterPro; IPR005123; 205.7 EMI Oxy. Ffam; PF03171; 20G-FeII Oxy; I. SEQUENCE 403 AA; 45431 MW; DE2CA70E6443A07C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 20.23
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338 YRTYNHGEYSRHYVTSR 354
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                                                                                                      124 EKYPMEP-----GGIQGYGHAFVFSDDQKLDWCNMLALGVEPAFIRRPNLWPTTPAN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 FSKTLEKÝSVEIRELCVRLLEHIAAALGLAPARLNGMFGEAVQAVRMNFYPPCPR---P 231
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                                                                        76 GF----TGLESESTAQITNTGSYSDYSMCYSMGT---ADNLFPSGD----FGRIWTQYFD 124
                                                                                                                                                                       125 RQYTASRAVAREVLRATGTEPDGGVEA-----FLDCEPLLRFRYFPQVPEHRSAEE-QP 177
                                                                                                                                                                                                                 133 DMFRLSKVLMRGFALALG-KPEDFFDAPLAEDDTLSAVSMIRYPYLEDYPPVKTGPDGTE 191
                                                                                                                                                                                                                                                                   178 LRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQ 237
                                                                                                                                                                                                                                                                                            64 IPVIDVGELQRGSEDELDNLRLACEQWGFFQVVNHGVEEETMEEMEKAARBFFMLPLEEK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
| : | | | | : | : | : | : | : | EINKACRGSGFFYASHHGI---DVQLLQDVVNEFHRTWIDEEKYDLAINAYNKANPHVRN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VPTFSLAELQQGLHQ--DEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 KRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGT-----ADNLFPS--GD
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37;
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9.4%; Score 154.5; DB 10; Length 366;
Best Local Similarity 22.1%; Pred. No. 5.8e-06;
Matches 70; Conservative 52; Mismatches 158; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAC
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STRAIN=CV. Nippombare;
Sasaki T., Matsumoto T., Yamamoto K.;
Subrite astiva nippombare(GA3) genomic DNA, chromosome 1, clone:P0492609.";
Submitteed (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001266; BAB64195.1; -.
Gramene; Q942Y0; -.
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PF03171; 20G-FeII Oxy; I.
4CE 366 AA; 40738 MW; 6EC44508E618458E CRC64;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                238 VKAPRHHV 245
                                                                                                                                                                                                                                                                                                                                                                                                             248 FPAPNHRV 255
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10 2942Y
AC 2942Y
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134 MFRLSKALMRGFALALG-KPEDFFDAPLSEADTLSAVSLIRYPYLEDYPPVKTGPDGTKL 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 GF----TGLESESTAQITNTGSYSDYSMCYSMGTAD--NLFPSGD----FGRIWTQYFDR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 GYYMAVKĞKKAVESWCYLNPSFTEDHPMIRSGAPLHEVNIWPDEKRHERFRPFCEQYYRD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 OYTASRAVAREVLRATGTEPDGGVEA-----FLDCEPLLRFRYFPQVPEHRSAEE-QPL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                      Palaniappan N., Seki T.;
"Phylogenetic relationship between the Isopenicillin N synthase (IPNS) and 16S rDNA genes.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB045852; BAB13300.1; --
HSSP; PO5326; 1BK0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 RMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces argenteolus.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                              Streptomyces hygroscopicus subsp. hygroscopicus.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=68042;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30112 MW; 449522395CF30653 CRC64;
                                                                                           01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Isopenicillin N synthase (IPNS) (Fragment).
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.4%; Score 154; DB 2;
24.7%; Pred. No. 4e-06;
262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isopenicillin N synthase (IPNS) (Fragment).
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InterPro; IPR005283; IPN_synth.
InterPro; IPR002057; ISopen N synth.
Pfan; PF03171; 20G-FeII Oxy; I.
PRINTS; PR00682; IPNS-WITHSE.
PROSITE; PS00185; IPNS-1; 1.
PROSITE; PS00186; IPNS_1; 1.
                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
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PRELIMINARY;
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Created)
PS00185, IPNS_1; 1. PS00186; IPNS_2; 1.
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     PROSITE; |
PROSITE; |
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                                                                                    The Palaniappan N., Seki T.;

The Palaniappan N., Seki T.;

The Palaniappan N., Seki T.;

Thylogenetic relationship between the Isopenicillin N synthase (IPNS) in the Polaniappan N. Submitted (Jul. 2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB045857; BAB13305.1; -.

REMBL; AB045857; BAB13305.1; -.

REMBL; AB045857; BAB13305.1; -.

REMBL; AB045857; BAB13305.1; -.

RICEPTO; IPR002283; IPN synth.

RICEPTO; IPR002057; Isopen N synth.

REAPTO; IPR002682; IPR0SYNTHASE.

REAPTO; PR00682; IPNSYNTHASE.

REAPTO; PR00185; IPNS 1; 1.

REAPTO; PR00185; IPNS 1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 RIWTQYFDRQYTASRAVAREVLRATGT----EPDGGVEAFLDCEPLLRFRYFPQVPEHR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 TGPDGTKLSFEDHLDVSMITVLFQTQVQN----LQVETVDGWQDLPTSEDNFLVNCGTYM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : : | | | : | : | : | : | CINKACKGSGFFYASHGI---DVQRLQDVVNEFHRTMSDQEKYDLAINAYNENNPHVRN 73
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Palaniappan N., Seki T.;
Palaniappan N., Seki T.;
Palaniappan N., Seki T.;
Phalaniappan N., Seki T.;
Phalaniappan N., Seki T.;
Submitted (Jun-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, PAB045865.
IRNO.;
PRO05123; 20G-FeII Oxy.
InterPro; IPR002583; IPN synth.
InterPro; IPR002057; Isopen N synth.
Pfam; PF03171; 20G-FeII Oxy.
Pfam; PF03171; 20G-FeII Oxy.
Pfam; PF03171; 20G-FeII Oxy.
Pfam; PF03171; 20G-FeII Oxy.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.4%; Score 154; DB 2; Length 262;
llarity 24.3%; Pred. No. 4e-06;
Conservative 32; Mismatches 115; Indels
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Isopenicillin N synthase (IPNS) (Fragment).
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262 AA;
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nes 62; Conserv
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                                                SEQUENCE FROM N.A.
  NCBI_TaxID=67274;
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92 GFFLVVNHGVDDKLIAHAHQYIDYFFELPMSAKQRA-----QRKVGEHCGYASSFTGR 144
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                                                                                                                                                                                                                                                                                                                                                                                      76 GF----TGLESESTAQITNTGSYSDYSMCYSMGT---ADNLFPSGD----FGRIWTQYFD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 RQYTASRAVAREVLRATGTEPDGGVEAPL---DCEPLLRFRYFPQVPEHRSAEEQP---- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQ 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 LSFQDHLDVSMITVLFQTEVQN----LQVETVDGWQDLPTSGDHFLVNCGTFMGYLTNDY 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQYFDRQYTA 129
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                                                                                                                                                                                                                                                                                       21 BFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEK-----RAVTSPVPTMRR
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Bukaryoch; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fagales; Fagaceae; Fagus.
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9.3%; Score 152; DB 10; Length 379;
Best Local Similarity 24.3%; Pred. No. 1e-05;
Matches 67; Conservative 40; Mismatches 105; Indels 6
                                                                                                      Length 262
                                                                                                      Query Match
9.3%; Score 152; DB 2; Length 26
Best Local Similarity 25.0%; Pred. No. 6.2e-06;
Matches 62; Conservative 39; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL, A4220192; CAD21846.1; -. InterPro; IPR05123; 2OG-FeII Oxy. InterPro; IPR05123; IPN synth. Pfam; PF01171; 2OG-FeII Oxy. Pran; PF0171; 2OG-FeII Oxy; 1. SEQUENCE 379 AA, 43056 MW; E3E51A2FC94EFBB3 CRC64;
262 262
262 AA; 30107 MW; D72BF9737CC8EAEB CRC64;
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Last annotation update)
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199 SLGIMELLGMSLGVSQGHYREFFEENESIMRLNYYPPCQKP-----DLTLGTGPHCDPT 252

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188 MVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIA	253 SLTILHQD	241 PRHHVAAPRRDQIAGSSRTSSVPFLRPNADFTFSVP 276	302 CLHRAVVNSKTPRKSLAFFLCPKNDKVVSPP 332	Search completed: February 3, 2004, 17:38:34 Job time : 44 Becs
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4, Appli 3, Appli 4, Appli 10, Appli 2, Appli 2, Appli 2, Appli 4, Appli 4, Appli 2, Appli 4, Appli 2, Appli 2, Appli 2, Appli 2, Appli 2, Appli 4, Appli

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Title: Perfect score:

Sequence:

protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence

Sequence 4, Sequence 4, Sequence 22; Sequence 26;

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PRHHVAAPRRDQIAGSGRISSVFFLRPNADFIFSVPLARECGFDVSLDGETATFQDWIGG 300
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                                                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/09413231

Patent No. 6284483

GENERAL INPORMATION:
APPLICANT: Dilley, David R

APPLICANT: Wang, Zhenyong

APPLICANT: Wang, Zhenyong

APPLICANT: Wang, Zhenyong

APPLICANT: Wang, Zhenyong

TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate

TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate

FILE REFERENCE: MSG41-453

CURRENT APPLICATION NUMBER: US/09/413,231

CURRENT APPLICATION NUMBER: US/09/413,231

CURRENT PILING DATE: 1999-10-06

NUMBER OF SEQ ID NOS: 18

SOOTWARE: PatentIn Ver. 2.0

SEQ ID NO 18

LENGTH: 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: modified DAOCS OTHER INFORMATION: from Streptomyces clavuligerus
NAME/KEY: MUTAGEN
LOCATION: (181)
                                                      US-09-645-168-3
US-09-645-168-3
US-09-27-064-4
US-09-451-1815-4
US-09-455-168-2
US-08-823-986A-2
US-08-823-986A-2
US-08-157-077-9
PCT-US92-08012-2
US-09-157-077-9
US-09-187-1885-4
US-09-252-991A-25599
US-09-252-991A-26105
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; OTHER INFORMATION: Ala181 in native DAOCS modified
US-09-413-231-18
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Pred. No. 2.3e-176;
0; Mismatches 2;
US-09-252-991A-20513
US-08-379-5568-4
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Best Local Similarity 99.4%;
Matches 309; Conservative
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Sequence 28503,
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Sequence 10,
Sequence 8, An
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Sequence 17
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Sequence 2
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/cgm2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
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/cgm2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
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                    GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-592-411-15
US-08-592-411-17
PCT-US55-04801-6
US-09-413-231-5
US-09-413-231-9
US-08-379-556A-10
US-08-379-556A-10
US-08-379-556A-2
US-09-413-231-4
US-09-413-231-4
US-09-295-306-6
US-09-295-306-6
US-09-413-231-1
US-09-413-231-2
US-09-413-231-2
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US-09-413-231-2
US-09-295-306-2
US-09-413-231-2
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US-09-295-306-2
US-09-295-306-4
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US-09-213-231-7
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Maximum Match 100%
Listing first 45 summaries
                                                                        using sw model
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seq length: 200000000
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241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQ 121
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                                                                                                                                                                                                                                                     Process for the Efficient Production of 7-ADCA via 2-(Carboxyethylthio)acetyl-7-ADCA and 3-(Carboxymethylthio)propionyl-7-ADCA
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                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISP Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 73.4%; Score 1201; DB 1; Best Local Similarity 70.3%; Pred. No. 3.3e-128; Matches 218; Conservative 41; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/592,411
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Fatent No. 5726032
GENERAL INFORMATION:
TITLE OF INVENTION: 7-ADCA via 2-((;)) TITLE OF INVENTION: 7-ADCA via 2-((;)) TITLE OF INVENTION: 3-(Carboxymeth); NUMBER OF SEQUENCES: 17
                                                                                                                                                                         Sequence 15, Application US/08592411
; Patent No. 5726032
; GENERAL INFORMATION:
; TITLE OF INVENTION: 7-ADCA via 2-(C)
; TITLE OF INVENTION: 7-ADCA via 2-(C)
; TITLE OF INVENTION: 3-(Carboxymeth);
; UMBER OF SEQUENCES: 17
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 313 amino acida
TYPE: amino acid
TOPOLOGY: linear
                                      301 NYVNIRRISKA 311
                                                                          301 NYVNIRRTSKA 311
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US-08-592-411-15
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US-08-592-411-17
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243 PKHHVAAPGADKRVGSSRTSSVFFLRPNGDFRFSVPRARECGFDVSIPAETATFDDWIGG 302:
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APPLICANT: Coque, Juan R.
APPLICANT: Coque, Juan R.
APPLICANT: Enguite, Francisco J.
APPLICANT: Llarena, Francisco J.
APPLICANT: Liras, Paloma
TITLE OF INVENTION: DATE GENES
NUMBER OP SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: John W. Wallen III
STREET: P.O. Box 2000
               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,411
FILING DATE:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52;
                                                                                                                                                                                                                                                                                                                                                                                                                                      72.5%; Score 1186.5; DB 1
69.8%; Pred. No. 1.5e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US95-04801-6; Sequence 6, Application PC/TUS9504801; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 69.8%
Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 NYVNIRRISKA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 NYINIRKTAAA 313
                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-592-411-17
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MEDIUM TYPE: Floppy
COMPUTER READABLE FORM:
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STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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14;

46; Gaps

99

215

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126 VNLWPDEERHPRFRPFCEGYYRQMLKLSTVLMRGLALALG-RPEHFFDAALAEQDSLSSV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 SLIRYPYLEEYPPVKTGPDGGLLSFRDHLDVSMITVLFQTQVQN----LQVETVDGWRDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 DNLFPSGD----FGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEA-----FLDCE 156
                                                                                                                                                                                                                                                                                                                   59 SEAEK----RAVTSPVPTMRRGF----TGLESESTAQITNTGSYSDYSMCYSMGT---A 106
                                                                                                                                                                                                                                                                                                                                                                                                                                              107 DNLFPSGD-----FGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVBA-----FLDCE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 PTSENDFLVNCGTYMAHVTNDYFPAPNHRV-----KFVNAERLSLPFFLNGGHEAVIE- 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 SEAEK----RAVISPVPIMRRGF----IGLESESTAQIINIGSYSDYSMCYSMGT---A 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 VPTIDISPLEGTDAAAKKRVAEEIHGACRGSGPFYATNHGV---DVQQLQDVVNBEHGAM 66
                                                                                                                                                                                                                            10 VPIDISPLFGTDAAAKKRVAEEIHGACRGSGFFYATNHGV---DVQQLQDVVNEFHGAM
                                                                                                                                                                                       5 VPTFSLAEL-----QQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 PLLRFRYFPQVPEHRSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 PYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSV
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Best Local Similarity 23.8%; Pred. No. 4.2e-10;
Matches 77; Conservative 50; Mismatches 150; Indels 46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description of Artificial Sequence: modified IPNS from Streptomyces clavuligerus strain NRRL 3585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/09413231
| Patent No. 6284483
| GENERAL INFORMATION:
| APPLICANT: Dilley, David R
| APPLICANT: Warner, Toni M
| APPLICANT: Warner, Toni M
| TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate FILE REFERENCE: MSU41-453
| CURRENT APPLICATION NUMBER: US/09/413,231
| CURRENT FILING DATE: 1999-10-06
| NUMBER OF SEQ ID NOS: 18
                                                        Length 329;
                                                        10.0%; Score 164; DB 3; Length 32; 23.8%; Pred, No. 4.2e-10; cive 50; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) LOCATION: (210)
; OTHER INFORMATION: Glu210 in native IPNS modified to Arg
US-09-413-231-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>..</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294 PFVPE-GASEEVRNEALSYGDYL 315
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                                                        Query Match
Best Local Similarity 23.84
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
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OTHER INFORMATION:
NAME/KEY: MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 9
LENGTH: 329
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US-09-413-231-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRMA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 EKQAVTTKVPIMRRGYSALEAESTAQVINTGTYTDYSMSYSMGIGGNLFPSKEFESVWTD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09413231
| Patent No. 6284483
| GENERAL INFORMATION:
| APPLICANT: Dilley, David R
| APPLICANT: Mang, Zhenyong
| APPLICANT: Wang, Zhenyong
| APPLICANT: Warner, Toni M
| TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
| TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
| TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
| TITLE OF STOWNION: Cephalosporins Under the Control of Sicarbonate
| TITLE OF STOWNION: Cephalosporins Under the Control of Sicarbonate
| TITLE OF STOWNION: Cephalosporins Under the Control of Sicarbonate
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| TITLE OF STOWNION: Cephalosporins Under the Control of Sicarbonate
| TITLE OF STOWNION: Cephalosporins Under the Control of Sicarbonate
| TITLE OF STOWNION: Cephalosporins Under the Control of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 59.0%; Score 965.5; DB 5; Best Local Similarity 61.2%; Pred. No. 2.1e-101; Matches 186; Conservative 37; Mismatches 80;
                                                                                   NAME: Wallen III, JOHN W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19179
TELECOMOUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-09-413-231-5
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163 YFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAV 222
                              205 YYPPCP----CPELALGVAPHTDMSSITIL----VPNEVQGLQVFKDGQWYDVAXIPNAL 256
                                                                                       223 LVFCGAIATLVTGGQVKAPRHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECG 282
                                                                                                                   257 IIHIGDQIEILSNGKYKSVYHRSTVNKE----KTRMSWPAFLEPPPEFEVG-PIPKLVN 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 FEHGSEAEKRAVTSPVPTWRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 EAFLDCEPLLRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 LDTVLEVPAIDLS----LEEDDVVKLVLSASKEWGLFQVTNHGIPTEVIEKLOKVGKMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 FGRIWT-----QYF------DRQYTASRAVAREVL-----RATGTEPDG-----GV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDTT--VPTFSLAELQQGLHQDEFRRCL----RDKGLFYLTDCGLTDTELKSAKDLVIDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.1%; Score 149; DB 2; Length 333; 21.6%; Pred. No. 2.2e-08; tive 57; Mismatches 126; Indels '
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: HOLTON, TIMOTHY A.
APPLICANT: HOLTON, TIMOTHY A.
APPLICANT: KEAM, LISA A.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOL
TITLE OF INVENTION: SYNTHASE ENZYMES AND USES THEREFORE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE S. 21
CORRESPONDENCE ADDRESS:
ADDRESSER: ACULLY SCOTT MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,556A FILING DATE: 22-MAR-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08379556A
Patent No. 5859329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 22-MAR-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLIO, FRANK S.
REFERATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (516)742-4343
TELEFAX: (516)742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                               283 FDVSLDGETATFQDWI 298
                                                                                                                                                                                                                           311 KDDPPKYKTKKYKDYV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 333 amino acids
amino acid
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Best Local Similarity 21.6%
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                 US-08-379-556A-8
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                                                157 PLLRFRYFPQVPEHRSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDL 215
                                                                                       185 SLIRYPYLEEVPPVKTGPDGQLLSFRDHLDVSMITVLFQTQVQN----LQVETVDGWRDI 240
                                                                                                                                   PYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSV 275
                                                                                                                                                                             241 PISENDFLVNCGIYMAHVINDYFPAPNHRV-----KFVNAERLSLPFFLNGGHEAVIE- 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 AVTSPVPTWRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLF-----PSGDFGRIW 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 VIAKP-----DGYKGVE-----GYGTKLQKEVQGKKGWVDHLFHIVWPPSFINYQFW 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 TQ----YFD--RQYTASR-AVAREVL----RATGTEPD-----GGVEAFLDCEPLLRFR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 VNLWPDEERHPRFRPFCEGYYROMLKLSTVLMRGLALALG-RPEHFBDAALAEODSLSSV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 VPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKR
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Sequence 10, Application US/08379556A

GENERAL INFORMATION:
APPLICANT: HOLTON, TIMOTHY A.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOL
TITLE OF INVENTION: SYNTHASE ENZYMES AND USES THEREFORE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: SCULLY SCOTT MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.9%; Score 162; DB 2; Length 335; Best Local Similarity 22.8%; Pred. No. 7.3e-10; Matches 72; Conservative 55; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 PLARECGFDVSLDGETATFQDWI 298
                                                                                                                                                                                                                                                    294 PFVPE-GASEEVRNEALSYGDYL 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9592
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516)742-4343
TELEFAX: (516)742-4346
TELEFAX: (516)742-4366
TELEY 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLIO, FRANK S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GARDEN CITY
NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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APPLICANT: HOLTON, TIMOTHY A.
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TYPE: amino acid
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TELEPHONE: (516)742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                 11530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-413-231-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 TEEDTLSCRSLMIRYPYLDPYPEAAIKTGPDGTRLSFRDHLDVSMITVLFQTEVQN---- 232
                                                                      242 GRWYDVXYIPNALIIHVGDQMEIMSNGEYKAVLHRSTVNKE----RTRISWPVFLEPPS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 GSEAEK-----RAVTSPVPTWRRGFTGLESESTAQITNTGSYSDYSMCY---SMGTADNL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 FPSG-----EPDGTIWTQYFDRQYTASRA-VAREVLRATGT-----EPDG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 IKAĞTPMHEVNVWPDEERHPDFRSFGEQYYREVFRLSKVLLLRGFALALĞKPEEFFENEV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 LOAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVF 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 LOVETVDGWOSLPTSGENFLINCGTYLGYLTNDYPPAPNHRV-----KYYNAERLSLPF 286
193 E---DIVYLLKINYYPPCPR----PDLALGVAAHTDLSVITIL----VPNDVAGLQVSRD 241
                                              210 GAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 VPTFSLAELQQGLHQD-----EPRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: modified IPNS OTHER INFORMATION: from streptomyces anulatus (S. lipmanii)
NAME/KEY: MUTAGEN
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dilley, David R
APPLICANT: Kadyrzhanova, Dina K
APPLICANT: Wang, Zhenyong
APPLICANT: Wang, Zhenyong
APPLICANT: Warner, Toni M
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
FILE REFERENCE: MSU41-453
CURRENT APPLICATION NUMBER: US/09/413,231
CURRENT FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PETENTIN Ver. 2.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64;
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8.7%; Score 143; DB 3; Length 333;
Best Local Similarity 23.2%; Pred. No. 1.1e-07;
Matches 70; Conservative 37; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (214)
OTHER INFORMATION: Glu214 in native IPNS modified to Arg
                                                                                                                                   270 DFTFSVPLARECGFDVSLDGETATFQDW 297
                                                                                                                                                                 | | | : : : | ::
297 DFAVG-PIPKLISDEKPAKYKTKVFSEY 323
                                                                                                                                                                                                                                            RESULT 9
US-09-413-231-10
; Sequence 10, Application US/09413231
; Patent No. 6284483
; GENERAL INFORMATION
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US-08-379-556A-2
; Sequence 2, Application US/08379556A
; Patent No. 5859329
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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85 TAQITUTGSYSDYSMCYSMGTADNLF----PSGDFGRIW-------TQYFDRQYT 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 ASRAVAREVLRATGTEPDGGVEAFLDCE--PLLRFRYFPQVPEHRSAEEQPLRMAPHYDL 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 RDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVT-SPVPTMRRGF-TGLESES
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Parent No. 6284483

GENERAL INFORMATION:
APPLICANT: Dilley, David R
APPLICANT: Kadyrzhanova, Dina K
APPLICANT: Warner, Toni M
APPLICANT: Warner, Toni M
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 347;
APPLICANT: TEAM, LISA A.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOL
TITLE OF INVENTION: SYNTHASE ENZYMES AND USES THEREFORE
CORRESPONDENCES: 2.1
ADDRESSEE: SCULLX SCOTT MURPHY & PRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                               COMPUTER TEXABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPPY disk
COMPUTER: PLOPPY DISK
COMPUTER: PLOPPY DISK
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,556A
FILING DATE: 22-MAR.1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

8.6%; Score 140; DB 2;
Best Local Similarity 22.3%; Pred. No. 2.5e-07;
Matches 59; Conservative 43; Mismatches 114
                                                                                                                                                                         ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER STREET: 400 GARDEN CITY PLAZA CITY: GANDEN CITY STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 APRRDQIAGSSRTSSVFFLRPNAD 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLO, FRANK S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 959
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 GSEAEKRAVISPVPIMRRGFIGLESESTAQ----IINIGSYSDYSMCY---SMGTADNLF 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 ----ESTIMIDQRSITWRSTRYNENNSHVRNGYYMARPGRETVESWCYLNPSFGEDHPMM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 PSG-----AREVLRATGTEPDGGV-- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 KAĞIPMHEVNVWPDEERHPDFGSFGEQY-HREVSASRRCCCGASRWRRQAĞESSSNEVTE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 EAFLDCEPLLRFRYFPQVPE---HRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 EVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLR 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 ETVDGWQSLPTSGENFLINCGTYLGYLTNDYFPAPNHRV-----KYVNAERLSLPFFLH 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 VPTFSLABLQQGLHQDEFR-----RCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEH 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 VPTIDISPOLFGTDPTPRRTSRGRSTRPARGSGFFYASHHGIDVRRLQTWSN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: modified IPNS; OTHER INFORMATION: from Penicillium chrysogenum; NAME/KEY: MUTAGEN; LOCATION: (212); LOCATION: (212); OTHER INFORMATION: Glu212 in native IPNS modified to Arg
                                                                                                                                                                                                                     FEATURE: OTHER INFORMATION: Description of Artificial Sequence: modified IPNS OTHER INFORMATION: from Streptomyces cattleya NAME/KEY: MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dilley, David R
APPLICANT: Dilley, David R
APPLICANT: Kadyzhanova, Dina K
APPLICANT: Warner, Zhenyong
APPLICANT: Warner, Toni M
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
FILE REFERENCE: MSU41-453
CURRENT APPLICATION NUMBER: US/09/413,231
CURRENT FILING DATE: 1999-10-06.
NUMBER OF SEQ ID NOS: 18
SOFTHARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               62;
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.4%; Score 137; DB 3; Length 321; Best Local Similarity 23.1%; Pred. No. 4.8e-07; Matches 73; Conservative 32; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                               ; LOCATION: (211)
; OTHER INFORMATION: Glu211 in native IPNS modified to Arg
US-09-413-231-8
FILE REFERENCE: MSU41-453
CURRENT PEPLICATION NUMBER: US/09/413,231
CURRENT FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 8
LENGTH: 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09413231
Patent No. 6284483
GENERAL INFORMATION:
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                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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LENGTH: 331
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US-09-413-231-4
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197 PAAIKTAEDGTKLSFRWHEDVSLITVLYQSDVAN----LQVEMPQGXLDIEADDNAYLVN 252
                                                                                                                                                                                                                                                                                                                                                                                137 GFREFABOYYWDVFGLSSALLRGYALALGKBEDFFSRHFKKEDALSSVVLIRYPYLNPIP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                           169 EH--RSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVF 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 CGSYMAHITINNYYPAPIHRV-----KWVNEERQSLPFFV--NLGFNDTVQPWDPSKEDG 304
                                                                                                                                                                                                                       61 -AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTAD--NLFPS----G 113
                                                                                                                                                                                                                                                                       94 IPEKKAVES------FCYL-----NPNFKPDHPLIQSKTPTHEVNVWPDEKKHP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGAIATLVTGGQVKAPRHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDV 285
                                                                                                                                                              37 RDTGFFYAVNHGVDVKRLSNKTREFHFSITDEE---KWDLAIRAYNKEHQDQIRAGYYLS 93
                                                                                                                                                                                                                                                                                                                                  114 DFGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAF----LDCEPLLRFRYFPQVP
                                                                                                           27 RDKGLFYLTDCG------LTDTELKSAKDLVIDFF--EHGSE----
                                                     Gaps
                                                  73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Theodor LANGE et al.
APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEGUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
  Length 331;
8.2%; Score 133.5; DB 3; Length 24.1%; Pred. No. 1.3e-06; tive 39; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Wenderoth, Lind & Ponack, L.L.P. 2033 K Street, N.W., Suite 800
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N: 800
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MEDIUM TYPE: Diskette, 3.5 inch, 1.44
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,367A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49/FD4.5MZ
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REGISTRATION NUMBER: 40,949
REFRENCE/DOCKET NUMBER: 49/F;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8250
TELEFAX: 202-721-8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
Query Match
Best Local Similarity 24.19
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: NO CLASSIFICATION:
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MOLECULE TYPE:
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                                                                                                                       CLONE:
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                                                                                                                                                                                                                                                   89 GFFLVVNHGVSESLIADAHRLMESFFDMPLAGKQKAQRKPGESCGYASSFTGRFSTKLPW 148
                                                                                                                                                                                                                                                                                                                              149 KETLSFQFSNDNSGSRTVQDYFSDTLGQEFE--QFGKVYQDYCEAMSSLSLKIMELLGLS 206
                                                                                                                                                                                                                                                                                                                                                                                   TGTEPDGGVEAFLDCEPLLRFRYFP--QVPEHRSABEQPLRMAPHYDLSMVTLIQQTPCA 198
                                                                                                                                                                                                                                                                                                       85 ----TAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQYFDRQYTASRAVAREVLRA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 NGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 NG---LQVFVDNQWQSIRPNPKAFVVNIGDTFMALSNGIFKSCLHRAVVNRB-----SAR 311
                                                                                                                                                                                                                        30 GLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVTSPVPT--MRRGFTGLESES---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-09-295-306-6
Sequence 6, Application US/09295306
Patent No. 61398021
GENERAL INFORMATION:
APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                28;
                                                                                                                                        Query Match 8.0%; Score 131, DB 2, Length 378, Best Local Similarity 23.3%; Pred. No. 3e-06; Matches 60; Conservative 40; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/553,367
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 49/DIV-FD4.5MZ
TELECOMMUNICATION:
TELECOMMUNICATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44
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; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; IMMEDIATE SOURCE:
; CLONE: zu pAT2353
US-08-553-367A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 TSSVFFLRPNADFTFSVP 276
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OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09,
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
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D.C.
T. U.S.A.
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US-09-295-306-6
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85 ----TAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQYFDRQYTASRAVAREVLRA 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 NG----LQVFVDNQWQSIRPNPKAFVVNIGDTFMALSNGIFKSCLHRAVVNRE-----SAR 311
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TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (AS Amended)
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                       Query Match 8.0%; Score 131; DB 3; Length 378; Best Local Similarity 23.3%; Pred. No. 3e-06; Matches 60; Conservative 40; Mismatches 130; Indels
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REPERENCE/DOCKET NUMBER: '2000-1678/LC/01784
TELECOMMUNICATION:
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P. STREET: 2033 K Street, N.W., Suite 800
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MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb COMPUTER: IBM COMPATER: TBM COMPATER: OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1
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APPLICATION NUMBER: 09/295,306
FILING DATE: April 21, 1999
APPLICATION NUMBER: 08/53,367
FILING DATE: NO. 6455675ember 27,
APPLICATION NUMBER: PCT/EP94/01664
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APPLICATION NUMBER: US/09/734,719
FILING DATE: 13-Dec-2000
CLASSIFICATION: «UNKNOWN»
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                                                                                                         ORGANISM: Arabidopsis thaliana IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09734719
Patent No. 6455675
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 TSSVFFLRPNADFTFSVP 276
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TELEX: <Unknown>
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COUNTRY: U.S.A.
ZIP: 20006
protein
NO
                                                                                                                                                          zu pAT2353
        MOLECCEL
HYPOTHETICAL: N
                                                      ANTI-SENSE: NO ORIGINAL SOURCE:
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85 ----TAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQYFDRQYTASRAVAREVLRA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 TGTEPDGGVEAFLDCEPLLRFRYFP--QVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 LGVNRDYPRGFFEENDSIMRLNHYPPCQTP-----DLTLGTGPHCDPSSLTILHQDH-V 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 NGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 NG---LÖVFVDNQMQSIRPNPKAFVVNIGDTFMALSNGIFKSCLHRAVVNRE----SAR 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 GLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVTSPVPT--MRRGFTGLESES--- 84
                                                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.0%; Score 131; DB 4; Length 378; Best Local Similarity 23.3%; Pred. No. 3e-06; Matches 60; Conservative 40; Mismatches 130; Indels 2
| INFORMATION FOR SEQ ID NO: 6:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 378 amino acids
| TYPE: amino acid |
| TYPE: amino acid |
| STRANDEDNESS: single |
| TOPOLOGY: linear |
| HYPOTHETICAL: NO |
| HYPOTHETICAL: NO |
| AMTI-SENSE: NO |
| ORGANISM: Arabidopsis thaliana |
| IMMEDIATE SOURCE: |
| CLONE: ZU PAT2353 |
| SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-734-719-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: February 3, 2004, 17:43:00 Job time : 22 secs
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Sequence 18, Appl
Sequence 12239, A
Sequence 5, Appli
Sequence 14043, A
Sequence 10, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 7939, A
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14020, A
12421, A
                                                                                                                    February 3, 2004, 17:36:38; Search time 33 Seconds (without alignments) 1973.269 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                              1637
1 MDTTVPTFSLAELQQGLHQD.....ATFQDWIGGNYVNIRRTSKA 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (gn2_6/ptodata/2/pubpaa/US07_PUBCOMB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.ppp:*
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(cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.ppp:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-924-841-9
US-10-369-93-14043
US-09-924-841-10
US-10-136-444-8
US-10-431-273-88
US-09-924-841-8
US-10-369-493-17939
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US-10-369-493-7649
US-10-369-493-14020
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US-10-369-493-4891
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US-10-369-493-12239
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                                                                                                                                                                                                                                                                                                                                                         801455 segs, 209382283 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maximum Match 100%
Listing first 45 summaries
                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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168
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148.5
148.5
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133.5
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128.5
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-369-493-19206 Sequence 3	aniente T-Tro	sednence	841-3 Sequence	-369-493-13125 Sequence	371-307-78 Seguence 78	Sequenc	Seque	US-10-221-296-2 Sequence 2, Appli	Seque	Seque	Sedne	Seque	Seque	Segue	23 Segue	e Segue	400 Seque	Seguen	321-59 Seque	3-7385 Segue	Segue	3-16772 Seque	3-22794 Seque	493-15764 Segue	493-16148 Sequence	0-369-493-15396 Seguence	-493-12622 Sequence	0-316-306-	0-289-757-124	
12 US-10	5 :	ő	ö	5	-60-Sn 6			12 US-10							12 US-10		7	-60-SN 6	US-1	US-1						US-1	US-1	4	US-1	
268	100	331	331	• •	•	386	269	377	373 1	345 1	258 1	309	311 1	338	369	338			321	296	306	311	335	299	299	303	336	361	380	
7.6								7.4								6.5	•		•	٠	•	٠	٠	•	•	•	٠	6.1	•	
124		227.5	122.5	122.5	122.5	122.5	122	120.5	119.5	119	118.5	110.5	109	109	109	106	104.5	104	104	103.5	103.5	103.5	100.5	100	100	100	100	99.5	66	
16	1 1	87	19	20	21	22	23	24	25	. 26	27	28	58	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

9 9 APPLICANT: Dilley, David R
APPLICANT: Mangy Zhenova, Dina K
APPLICANT: Wangy Zhenova, Dina K
APPLICANT: Wangy Zhenova,
APPLICANT: Wangy Zhenova
APPLICANT: Warner, Toni M
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
TITLE OF INVENTION: Modified Synthetases US/09/924,841
CURRENT FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 18
LENGTH: 311
TYPE: PRT
MANGHARE: PRT
MAN 1 MDTTVPTFSLAELQQGLHQDBFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE 1 MDTIVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTBLKSAKDLVIDFFEHGSE FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: modified DAOCS
OTHER INFORMATION: from Streptomyces clavuligerus
NAME/KEY: MUTAGEN ö Length 311; LOCATION: (181)
; OTHER INFORMATION: Ala181 in native DAOCS modified to Arg Indels 99.2%; Score 1624; DB 10; 99.4%; Pred. No. 3.5e-172; tive 0; Mismatches 2; Sequence 18, Application US/09924841; Patent No. US20020127633A1; GENERAL INFORMATION: Query Match Best Local Similarity 99.4 Matches 309; Conservative US-09-924-841-18 ठ 요

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4891, Ap

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SEQ ID NO 5
LENGTH: 329
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Gladmai, Barry S.
APPLICANT: Gladmai, Barry S.
APPLICANT: Goldmai, Barry S.
APPLICANT: Goldmai, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION NUMBER: US 10/10/369, 493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 RPHYDLSMYTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLYTGGQVKA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 EHGSEAEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 AL-PEADKLAIEMVKSSQFRGYTRAGGELTK-----GREDWREQLDIGVERQAIAQGPG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 GRIWTQ-YFDRQYTAS------RAVAREVLRATGTEPDGGVEAFLDCEPLL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 RFRYFPQVPEHR-SAEEQPLR------MAPHYDLSMVTLIQQTPCANGFVSLQAEVGG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 ----YSSEPNHRMKIVRYPGRDTTGGDQGVGAHKDGGFLTLLLQ----DDNKGLQVDYDG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 AFTDLPYRPDAVLVFCGALATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNAD 270
61 AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWT 120
                          61 AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFERIWT 120
                                                                            OYFDROYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRM 180
                                                                                                     121 QYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRM 180
                                                                                                                                                         181 APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA 240
                                                                                                                                                                                                                                         PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
                                                                                                                                                                                                                                                                241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDTTVPTFSLAELQQGLHQ-----DEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 FT----FSVPLARECGFDVSLDGETATFQDWIGGNYVNIRRTS 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12239, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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24.7%;
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ORGANISM: Mesorhizobium loti
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les 85; Conserv
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59 SEAEK----RAVTSPVPTMRRGF----TGLESESTAQITNTGSYSDYSMCYSMGT---A 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 PLLRFRYFPQVPEHRSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDL 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 VNLWPDEERHPRFRPFCEGYYRQMLKLSTVLMRGLALALG-RPEHFFDAALAEQDSLSSV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                GENERAL INFORMATION:

APPLICANT: Dilley, David R

APPLICANT: Dilley, David R

APPLICANT: Wang, Zhenyong

APPLICANT: Wang, Zhenyong

APPLICANT: Wang, Zhenyong

TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and

TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate

FILE REFERENCE: MSU41-453

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICANTON NUMBER: US/09/413,231

PRIOR FILING DATE: 1999-10-06

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 VPTFSLAEL-----QQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 VPÍIDISPLFGTDAAAKKRVAEEIHGACRGSGFFYATNHGV---DVQQLQDVVNEFHGAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: modified IPNS
OTHER INFORMATION: from Streptomyces clavuligerus
NAME/KEY: WITAGEN
LOCATION: (210)
COTHER INFORMATION: Glu210 in native IPNS modified to Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09924841
Sequence 9, Application US/09924841
Patent No. US20020127633A1
GENERAL INFORMATION:
APPLICANT: Ediley, David R
APPLICANT: Kadyrzhanova, Dina K
APPLICANT: Wang, Zhenyong
APPLICANT: Warner, Toni M
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate FILE REPERENCE: MOUAL-453
CURRENT APPLICATION NUMBER: US/09/924,841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
10.0%; Score 164; DB 10;
Best Local Similarity 23.8%; Pred. No. 2.3e-09;
Matches 77; Conservative 50; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 PLARECGFDVSLDGETATFQDWI 298
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Sequence 5, Application US/09924841 Patent No. US20020127633A1
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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 FPSG-----EPDGTIWTQYFDRQYTASRA-VAREVLRATGT----EPDG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 IKAGTPMHEVNVWPDEERHPDFRSFGEQYYREVFRLSKVLLLRGFALALGKPEEFFENEV 176
                                                                                                                            60 EAEKRAVTSPVPTWRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIW 119
                                                                                                                                                                        60 DSEKNAVGMINSPHFRGYNRAASEITR-----GQPDQREQFDLGAERDVLPLNADSPLW 113
                                                                                                                                                                                                                         120 TQ-----TEPDGGVEAFLDCEPLL 159
                                                                                                                                                                                                                                                                                                                              160 RFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEV-GGAFTDLPYR 218
                                                                                                                                                                                                                                                                                                                                                                             13 HIKLMRYPGQASTASNQ--GVGAHKDSGFLSFLLQDQQA----GLQVEIEEGRWIDALPR 226
                                                                                                                                                                                                                                                                                                                                                                                                                              219 PDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNAD----FTF 273
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                                                                     1 LPILDLSLLDGTPSQRQAFLDDLRHAARDVGPPYLTGHGIDAGLLEQVQDYARQFPAL-P 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09924841

Parent No. US20020127633A1

GENERAL INFORMATION:
APPLICANT: Dilley, David R

APPLICANT: Wang, Zhenyong

APPLICANT: Wang, Zhenyong

APPLICANT: Warner, Toni M

TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
FILLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
FILLE PERFENCE: MGV41-453

CURRENT APPLICATION NUMBER: US/09/924,841

CURRENT APPLICATION NUMBER: US/09/413,231

PRIOR APPLICATION NUMBER: US/09/413,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 VPTFSLAELQOGLHQD-----EFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEH
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                         ---OGGLHODEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
PRATIUS:
OTHER INFORMATION: Description of Artificial Sequence: modified IPNS
OTHER INFORMATION: from streptomyces anulatus (S. lipmanii)
NAMESTRY: MUTAGEN
LOCATION: (214)
OTHER INFORMATION: Glu214 in native IPNS modified to Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.7%; Score 143; DB 10; Length 333; 23.2%; Pred. No. 5.1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274 SVPLARECGFDVSLDGETATFQDWIGGNYVNIRRTS 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 333
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                               5 VPTFSLAEL-
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Matches
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; Publication No. US20030233675A1
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Goldman, Barry S.
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10 (52052) B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2002-02-28
; SEQ ID NOS: 47374
; SEQ ID NO 14043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 VNLWPDEERHPRFRPFCEGYYRQMLKLSTVLMRGLALALG-RPEHFDAALAEQDSLSSV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLIRFRYPPOVPEHRSAER-OPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSV 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 SEAEK-----RAVISPVPTMRRGF----TGLESESTAQITNIGSYSDYSMCYSMGT---A 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 DNLFPSGD----FGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEA-----FLDCE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 PISENDFLVNCGTYMAHVINDYFPAPNHRV-----KFVNAERLSLPFFLNGGHEAVIE- 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 VPTFSLAEL-----QQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: modified IPNS OTHER INFORMATION: from Streptomyces clavuligerus strain NRRL 3585 IAMEMEKEY: MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
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                                                                                                                                                                                                                                                                                                                                                                                                                           10.0%; Score 164; DB 10; Length 329; 23.8%; Pred. No. 2.3e-09; tive 50; Mismatches 150; Indels 4
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23.8%; Pred. No. 1.2e-07;
tive 43; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Glu210 in native IPNS modified to Arg
US-09-924-841-9
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US/09/413,231
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 9
LENGTH: 329
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ORGANISM: Pseudomonas fluorescens
                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 23.8%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80; Conservative
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Best Local Similarity
Matches 80; Conserva
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US-10-369-493-14043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 RGFFRLPITAKQQYANLP----RTYEGYGSRVGVQKGGPLDWGDY---YFLHLAPDAGK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 SGDFGRIWTQYFDRQYTASRAVAREVLR------ATGTEPDGGVEAF--LDCEPL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 SPD--KYWPTNPAICKDVSEEYGREVIRLCELLMKVMSASLGLEATRFQEAFGGSECGVC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 LRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 PDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || :| | | ::: |: || ::: |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || 
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Patent No. US20020127633A1

GENERAL INFORMATION:

APPLICANT: Dilley, David R

APPLICANT: Wang, Zhenyong

APPLICANT: Wang, Zhenyong

APPLICANT: Warner, Toni M

TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and

TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate

FILE REFERENCE: MSU41-453

CURRENT APPLICATION NUMBER: US/09/924,841

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US/09/413,231

PRIOR APPLICATION NUMBER: US/09/413,231

PRIOR PLING DATE: 1999-10-06

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDTTVPTPSLABLQQGLHQDEFR-----RCLRDKGLFYLTDCGLTDTELKSAKDLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.5%; Score 139.5; DB 12; Length Best Local Similarity 23.3%; Pred. No. 1.5e-06; Matches 70; Conservative 43; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to Arg
                               TITLE OF INVENTION: Compositions isolated from forage TITLE OF INVENTION: grasses and methods for their use. FILE REFERENCE: 11000-10650 CURRENT FILING DATE: 2003-05-06 NUMBER OF SEQ ID NOS: 92 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 88 LENGTH: 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
8.4%; Score 137; DB 10;
Best Local Similarity 23.1%; Pred. No. 2.3e-06;
Matches 73; Conservative 32; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (211)
OTHER INFORMATION: Glu211 in native IPNS modified
Forster, Richard L. S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-431-273-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-924-841-8
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APPLICANT: WUIR, Shelbagh R.
APPLICANT: TUNEN van, Adrianus J.
APPLICANT: VERHOBYEN, Martine E.
APPLICANT: OF INVENTION: APPLICANT ON THE FLAVONOID CONTENT OF A PLANT AND PLA
TITLE OF INVENTION: OBTAINABLE THEREBY
FILE REFERENCE: 056159-5106
CURRENT FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: EP 01304009.2
PRIOR APPLICATION NUMBER: EP 01304009.2
NUMBER OF SEQ ID MOS: 45
SOFTWARE: Patentin Ver. 2.1
177 TEEDTLSCRSLMIRYPYLDPYPEAAIKTGPDGTRLSFRDHLDVSMITVLPQTEVQN---- 232
                                                                                                                      LQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVF 263
                                                                                                                                                                                            233 LOVETVDGWOSLPTSGENFLINCGTYLGYLTNDYFPAPNHRV-----KYVNAERLSLPF 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --TQYFDRQYT 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 ASRAVAREVLRATGTEPDGGVEAFLDCE--PLLRFRYFPQVPEHRSAEEQPLRMAPHYDL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 VVDRIFKSLSLGLGLEGHEMIEAAGGDEIVYLLKINYYPPCPR----PDLALGVVAHTDM 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 SMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 SYITIL----VPNEVQGLQVFKDGHWYDVKYIPNALIVHIGDQVEILSNGKYKSVYHRTT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      th 8.6%; Score 140; DB 15; Length 359; Similarity 22.3%; Pred. No. 1.2e-06; 59; Conservative 43; Mismatches 114; Indels 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Demmer, Jeroen
APPLICANT: Shenk, Michael Andrew
APPLICANT: Glenn, Matthew
APPLICANT: Goo. US2030337108Alriss, Michael Geoffrey
APPLICANT: Saulsbury, Keith Martin
APPLICANT: Hall, Claire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 TAQITNTGSYSDYSMCYSMGTADNLF----PSGDFGRIW-
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US-10-431-273-88
US-10-431-273-88
; Sequence 88, Application US/10431273
; Publication No. US20030237108A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/10136444 Eublication No. US20030101477A1 GENERAL INFORMATION:
APPLICANT: COLLIVER, Steven P. APPLICANT: HUGHES, Stephen G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Petunia hybrida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                           FL 265
                                                                                                                                                                                                                                                                                                                                                  287 FL 288
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                                                                                                                                                                                                                                                                           264
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLB OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 IPEKKAVES------FCYL-----NPNFKPDHPLIQSKTPTHEVNVWPDEKKHP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 -AEKRAVTSPVPTWRRGFTGLESESTAQITNTGSYSDYSMCYSMGTAD--NLFPS----G 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 GFREFAEQYYWDVFGLSSALLRGYALALGKEEDFFSRHFKKEDALSSVVLIRYPYLNPIP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 EH--RSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVF 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 PAAIKTAEDGTKLSFRWHEDVSLITVLYQSDVAN----LQVEMPQGYLDIEADDNAYLVN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 CGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDV 285
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                                                                    Sequence 4, Application US/09924841

Patent No. US20020127633A1

GENERAL INFORMATION:

APPLICANT: Dilley, David R

APPLICANT: Madyrzhanova, Dina K

APPLICANT: Warner, Toni M

TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and

TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and

TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and

TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and

TITLE OF INVENTION: MODIFIED SPOINTS US/09/924,841

CURRENT APPLICATION NUMBER: US/09/924,841

FILE REPERENCE: MSU41-453

CURRENT APPLICATION NUMBER: US/09/413,231

PRIOR APPLICATION NUMBER: US/09/413,231

PRIOR APPLICATION NUMBER: US/09/413,231

PRIOR APPLICATION NUMBER: US/09/413,231

SEQ ID NO 4

LENGTH: 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 DFGRIWTOYFDRQYTASRAVAREVLRATGTEPDGGVEAF----LDCEPLLRFRYFPQVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 RDKGLFYLTDCG-------LTDTELKSAKDLVIDFF--EHGSB-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: modified IPNS
OTHER INFORMATION: from Penicillium chrysogenum
INAME/KEY: MUTAGEN
LOCATION: (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73;
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8.2%; Score 133.5; DB 10; Length 331;
Best Local Similarity 24.1%; Pred. No. 5.8e-06;
Matches 77; Conservative 39; Mismatches 131; Indels 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Glu212 in native IPNS modified to Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7649, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 SLDGETATFQDWIGGNYVNI 305
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APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Glodman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
FILE REFERENCE: 38-10(52052)8
FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                             177 EDTLSAVSMIRYPYLDPYPEAAIKTGPDGTRLSFRDHLDVSMITVLSKTEVQN----LQV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 EVGCAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLR 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETVDGWQSLPTSGENFLINCGTYLGYLTNDYFPAPNHRV-----KYVNAERLSLPFFLH 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 QTPCANGFVSLQAEVGG-AFTD----LPYRP--DAVLVFCGAIATLVTGGQVKAPRHHV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 GSEAEKRAVTSPVPTMRRGFTGLESESTAQ----ITNTGSYSDYSMCY---SMGTADNLF 110
                                                                                                                                                        --DEGRIWTQYFDRQYTASRAV---AREVLRATGTEPDGGV-- 149
                                                                                                                                                                                                                                                                                             118 KAGTPMHEVNVWPDEERHPDFGSFGEQY-HREVSASRRCCCGASRWRRQAGESSSNEVTE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 NTGSYSDYSMCYSMG-----TADNLFPSGDFGRIWTQYFDRQYTASRAVAREV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRAT----GTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VPTFSLAELQQGLHQDEFR-----RCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEH 57
                                                                                                                                                                                                                                                                                                                                                     EAFLDCEPLLRFRYFPQVPE---HRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 GLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVTSPVPTMRRGFTGLESESTAQIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
                                                       10 VPTIDISPOLFGTDPTPRRTSRGRSTRPARGSGFFYASHHGIDVRRLQTWSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.3%; Score 136.5; DB 12; 25.2%; Pred. No. 1.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 AAPRRDQIAGSSRTSSVFFLRPNADF 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 VNPPAER-RGHSRYSMPFFLHPAPDF 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17939, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 PNADFTFSVPLARECG 282
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Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 17939
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US-10-369-493-17939
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US-10-369-493-17939
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slacer, Steven C.
APPLICANT: Slacer, Steven C.
APPLICANT: Sladman, Barry S.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILL OF INVENTION: DLANTS WITH IMPROVED PROPERTIES
FILL SPERENCE: 38-10(52052)8
CURRENT FILLNG DATE: 2003-02-28
PRIOR FILLNG DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-21
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        84 IATEQ----LDPDKPSDLKETFDMG----LHLPADHPEVLAVKPLRGPNRHPAIPGWETL 135
                                                                                                                                 123 FDROYTASRAVAREVLR----ATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPL 178
                                                                                                                                                                                                  194 GAGAHTDYGCITLLYQ-DAAGG---LQVKNVKGQWIDAPPIDGTFVVNLGDMMARWSNDR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 RXSYIPSPLFITRTSTXLGFVLXYSATAAPQTESNSLTSTTREWNDPSRIPTCLHPFMDE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 ITAFCNYLTQSVNRRLLTLFSRVLELPDDYLWENVQSHGFPTGEGYFRHALFRPVQKETQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|| | :| :| :| | :: || | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | | :: || | :: || | | :: || | :: || | | :: || | | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || :: || | :: || | :: || | :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: 
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                                                                                                                                                                                                                                                                                                          179 RMAPHYDLSMVTLIQQTPCANGFVSLQAE-VGGAFTDLPYRPDAVLVFCGAIATLVTGGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 VKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNAD 270
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; DOTHER INFORMATION: unsure at all Xaa locations

US-10-369-493-12421
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Publication No. US20030233675A1
GENERAL INFORMATION:
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; Sequence 4891, Application US/10369493
; Publication No. US20030233675A1
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NAME/KEY: unsure
LOCATION: (1)..(3
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 HGSEAEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGD-- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --FGRI-----WTQYFDR-----QYTASRAVAREVLRAT----GTEPDGGVEAFLDC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 VLAGQALRGPNNWPDFMPELRPALYGYYEAVGACGADLLRAVAVSLGVEEQFFAPRYTKR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 EPLLRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDL 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ...-wTQY 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 128.5; DB 12; Length
; Pred. No. 1.9e-05;
43; Mismatches 161; Indels
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1 Similarity 22.7%; Pred. No. 2.3e-05;
62; Conservative 39; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 LESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276 PLARECGFDVSLDGETATFQDWIGGNYV 303
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/360,039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Burkholderia cepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.8%;
Best Local Similarity 21.6%;
Matches 71; Conservative 4
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NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14020
LENGTH: 320
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Best Local Similarity
Matches 62; Conserv
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US-10-369-493-14020
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ORGANISM:
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APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR PLILING DATE: 2003-02-28
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 4891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 RPDAVLVFCGALATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 SEAEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGD---- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 FGRI-----WTQYFDR-----QYTASRAVAREVLRAT----GTEPDGGVEAFLDCEP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |: | : | : | : | 1.2 AGQALRGPNNWPDFMPELRPALYGYCEAVGACGADLLRAVAVSLGVEEQFFAPRYTKRMQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 LLRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 VEGSFVVNVGDILLARWINDRFRSTLHRVI-----NASGRERYSIATFYDP----TYG--- 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 IPIIDLAGVRAGDPQALQRVAQEIREACTTIGFFYIVNHGVPQALIDAAAQAARRFFAFP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 VPTFSLABLOOGLHQ-----DEFRECLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       7.6%; Score 124.5; DB 12; Length 317; 21.5%; Pred. No. 5.5e-05; tive 43; Mismatches 160; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: February 3, 2004, 17:42:26
Job time : 34 secs
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                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-369-493-4891
Cao, Yongwei
Hinkle, Gregory J.
Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 21.5<sup>1</sup>
Matches 70; Conservative
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6/ptodata/1/paa/USu9% COMB.pep:-
6/ptodata/1/paa/US099A_COMB.pep:*
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2.6/ptodata/1/paa/US101_COMB.pep:*
12_6/ptodata/1/paa/US101_COMB.pep:*
n2_6/ptodata/1/paa/US101_COMB.pep:*
n2_6/ptodata/1/paa/US104_COMB.pep:*
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14: (cgn2 6 ptodata/l/paa/USO9_COMB.pep:*
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6/ptodata/1/paa/US09_COMB.pep:*
6/ptodata/1/paa/US091_COMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Perfect score:
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Query Match Length DB

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Result No.

Description

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APPLICANT: BALDAD, Matthew D.
APPLICANT: LLOYD, Matthew D.
APPLICANT: HARLOS Karl
APPLICANT: APPLICANT: AND SCHELTINGA, Anke S.
APPLICANT: APPLICANT: TERMISSCHA VAN SCHELTINGA, Anke S.
APPLICANT: VALEGARD, Karin
APPLICANT: TATLE CONTRAINENTION: X-RAY STRUCTURE
TITLE OF INVENTION: X-RAY STRUCTURE
FILE REPREBENCE: 08004624
CURRENT PILING DATE: 2000-06-23
FRIOR APPLICATION NUMBER: 9727370.0
FRIOR FILING DATE: 1997-12-24
FRIOR FILING DATE: 1997-12-24
FRIOR PRILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PATCHILIN Ver: 2.1
  Sequence 32088, A Sequence 11094, A Sequence 18, Appl Sequence 121286, Sequence 6, Appli Sequence 6, Appli Sequence 10913, A
                                                                                                                                                                                             Sequence 4796, Ap
Sequence 89857, A
Sequence 9085, Ap
Sequence 12239, A
Sequence 89855, A
Sequence 6, Appli
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Sequence 50491, A
Sequence 50490, A
Sequence 15162, A
Sequence 18920, A
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Sequence 4795, Ap
Sequence 94436, A
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Sequence 148589,
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US-09-791-537-32088
US-09-791-537-32088
US-09-794-847-18
US-09-794-847-18
US-09-794-847-18
US-09-794-847-18
US-09-794-537-11094
US-08-237-10913
US-09-791-537-10913
US-09-791-537-10914
US-09-791-537-94436
US-09-791-537-94436
US-09-791-537-9485
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US-09-708-427-50491
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GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FAPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE PATENTIN VERSION 3.0
SEQ ID NO 11094
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  PRHHVAAPRRDQIAGSSRISSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
                     241 PRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGG 300
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APPLICANT: Kadyrzhanova, Dina K
APPLICANT: Kadyrzhanova, Dina K
APPLICANT: Wang, Zhenyong
APPLICANT: Warner, Toni M
TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
FILE REFERENCE: MSU41-453
CURRENT APPLICATION NUMBER: US/09/924,841
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US/09/413,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 99.4%; Score 1627; DB 22; Length 311; Best Local Similarity 99.4%; Pred. No. 1.2e-177; Matches 309; Conservative 1; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Streptomyces clavuligerus
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108-09-24-841-18
Sequence 18, Application US/09924841
GENERAL INFORMATION:
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                                                                                 301 NYVNIRRISKA
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US-09-791-537-11094
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                                                                                   Length 311;
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                                                                                                                         0; Indels
                                                                                 Score 1637; DB 19;
Pred. No. 8.5e-179;
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Pred. No. 7.1e-178;
0; Mismatches 1;
                                                                                                                         0; Mismatches
  ; TYPE: PRT
; ORGANISM: Streptomyces clavuligerus
US-09-582-486-1
                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 311; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.7%;
Matches 310; Conservative
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; ORGANISM: pdb 1DCS
US-09-791-537-32088
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63 AEKKAVMTPIPTIRRGYAGLESESTAQITNTGKYTDYSMSYSMGTADNLFPSAEFEKAWE 122
                                                                         121 QYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYPPQVPEHRSAEEQPLRM 180
                                                                                                     181 APHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Coque, Juan R.
APPLICANT: Enguita, Francisco J.
APPLICANT: Puente, Juan L.
APPLICANT: Llarena, Francisco J.
APPLICANT: Liras, Paloma
AITLE OF INVENTION: DAM BNCODING CEPHAMYCIN BIOSYNTHESIS
TITLE OF INVENTION: LATE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/233,605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08233605
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: John W. Wallen III
STREET: P.O. Box 2000
CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Wallen III, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19
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TELEPRONE: (908) 594-3905
TELEPAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Martin, Juan F.
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Matches 186; Conservative
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303 NYINIRKTAAA 313
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 QYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRM 180
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                                                                                                                                                                     FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: modified DAOCS
OTHER INFORMATION: from Streptomyces clavuligerus
NAME/KEY: MUTAGEN
LOCATION: (181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.5%; Score 1186.5; DB 22; Length 314; 69.8%; Pred. No. 7.1e-127; ive 41; Mismatches 52; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                        Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                   ; LOCATION: (181)
; OTHER INFORMATION: Ala181 in native DAOCS modified to Arg
US-09-924-841-18
                                                                                                                                                                                                                                                                                                                                                                   Query Match 99.2%; Score 1624; DB 24; Best Local Similarity 99.4%; Pred. No. 2.7e-177; Matches 309; Conservative 0; Mismatches 2;
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GENERAL INPORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
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US-09-791-537-121286
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Best Local Similarity 69.8%;
Matches 217; Conservative 4
                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
     PRIOR FILING DATE: 1999-10-06
                           NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 311
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US-09-791-537-121286
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TYPE: PRT
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Sequence 10937, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
TITLE OF INVENTION: WETHOOS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FILING DATE: 2001-02-22
CURRENT FILING DATE: 2001-02-22
SOFTWARE: Patentin version 3.0
SEQ ID NO 10913
LENGTH: 310
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DTIVPTESLAELQOGLHQDEFRRCLRDKGLFYLTDCGLTDTBLKSAKDLVIDFFEHGSEA 61
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; ORGANISM: Streptomyces lactamdurans
US-09-791-537-10913
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   EKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQ 121
                                 62 BKQAVITKVPIMRRGYSALEAESTAQVINIGIYIDYSMSYSMGIGGNLFPSKEFESVWID 121
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GENERAL INFORMATION:
APPLICANT: Martin, Juan F.
APPLICANT: Enguita, Francisco J.
APPLICANT: Fuence, Juan L.
APPLICANT: Pleare, Juan L.
APPLICANT: Liras, Paloma
TITLE OF INVENTION: LATE GENES
NUMBER OF SEQUENCES: 8
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: BEATON DAIN:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,468
FILING DATE: 22-OCT-1996
CLASSIFICATION NUMBER: 08/233,605
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wallen INI, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19179
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: John W. Wallen III STREET: P.O. Box 2000 CITY: Rahway STATE: New Transfer N
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TELEFAX: (908) 594-3720
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino
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STRANDEDNESS: single
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US-08-727-468-6
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APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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                  122 YFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRMA
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                                                                                                                                                                                                                                                          242 RHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 94436, Application US/09791537 GENERAL INFORMATION:
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Best Local Similarity 56.7°
Matches 177; Conservative
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301 GNYVNMRRDKPA 312
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US-09-791-537-94436
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LENGTH: 332
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                                                                    APPLICANT: Bionomix, Inc.
APPLICANT: Bonomix, Inc.
APPLICANT: Bonomix, Inc.
APPLICANT: Bobe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION WOMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 10914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4795, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXRAVISPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YFDRQYTASRAVAREVLRATG---TEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RMAPHYDLSMYTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 DITVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                              57.4%; Score 939.5; DB 22; Length 318; 58.6%; Pred. No. 2.1e-98; ive 43; Mismatches 81; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.2%; Score 937; DB 22;
58.0%; Pred. No. 4.1e-98;
iive 45; Mismatches 83;
                                   Sequence 10914, Application US/09791537 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptomyces clavuligerus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Lysobacter lactamgenus US-09-791-537-4795
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 58.6
Matches 180; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.2
Best Local Similarity 58.0
Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGNYVNI 305
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RESULT 9
US-09-791-537-10914
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US-09-791-537-4795
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TYPE: PRT
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DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
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                                                                                                                                                                                                                                                                                                                      126 VNLWPDEEKHPRFRPFCEDYYRQLLRLSTVIMRGYALALGRREDPFDEALAEADTLSSVS 185
                                                                                                                                                                                                                                                                                                                                                                                                                               186 LIRYPYLEEYPPVKTGADGTKLSFEDHLDVSMITVLYQTEVQN----LQVETVDGWQDIP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 -SG---DFGRIW-----TQYFDRQYTASRAVAREVLRATGTEPDGGVEA--- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 ---FLDCEPLLRFRYFPQVPEHRSAEE-QPLRMAPHYDLSMVTLIQQTPCANGFVSLQAE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 LADTLSAVTLIHYPYLEDYPPVKTGPDGTKLSFEDHLDVSMITVLFQTEVQN----LQVE 232
                                                                                                                                                           58 GSEAEK-----RAVISPVPIMRRGF----IGLESESTAQIINIGSYSDYSMCYSMGTAD- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
                                                                                   10 VPIDISPLSGDDAXAKQRVAQ-EINKAARGSGFFYASNHGV---DVQLLQDVVNEFHRN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 TADGWQDLPTSGENFLVNCGTYMGYLTNDYFPAPNHRV-----KFINAERLSLPFFL 284
                                                                                                                                                                                                                                                                                                                                                                          LLRFRYFPQVPEHRS-AEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 VPTFSLABLOOGLHOD-----EFRRCLRDKGLFYLTDCGLTDTBLKSAKDLVIDFFEHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 VPIIDISPLSGGDADDKKRVAQEINKACRESGFFYASHHGI----DVQLLKDVVNEFHRTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 SEAEK-----RAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFP--
                                                    ---AELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEH
42; Gaps
                                                                                                                                                                                                                                                                    108 -NLFPSGD----FGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 YRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 RSDEDFLVNCGTYMGHITHDYFPAPNHRV-----KFINAERLSLPFFL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 329;
72; Conservative 45; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.8%; Score 176; DB 22; 24.5%; Pred. No. 2.2e-10; iive 39; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9085, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bloomaix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTUR:
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: MUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 9085
LENGTH: 329
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; Sequence 12239, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ; ORGANISM: Streptomyces griseus US-09-791-537-9085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 24.5
Matches 73; Conservative
                                                    5 VPTFSL---
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US-09-791-537-9085
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Matches
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPRENCE: 261/210
CURRENT APPLICATION UMBER: US/09/791,537
CURRENT APPLICATION UMBER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 89857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 GSEAEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGR 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQ 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 NRMAPHYDLSIVSLILQTPCPNGFVSLQVEIDGRFVEVPPRPGCVVVFCGSIAPLVSDGK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDW 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 313;
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Pred. No. 9.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 52.0%; Score 852; DB 22; Best Local Similarity 52.9%; Pred. No. 2.5e-88; Matches 165; Conservative 48; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 89857, Application US/09791537
GENERAL INFORMATION:
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; ORGANISM: Streptomyces jumonjinensis
US-09-791-537-89857
                                                                                                         Sequence 4796, Application US/09791537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Lysobacter lactamgenus
US-09-791-537-4796
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24.9%;
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Best Local Similarity
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US-09-791-537-89857
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APPLICANT: Slater, Steven C.
APPLICANT: Gladman, Barry S.
APPLICANT: Gladman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369, 493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12239
LENGTH: 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 ----YSSEPNHRMKIVRYPGRDTTGGDQGVGAHKDGGFLTLLLQ----DDNKGLQVDXDG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 SWYDVDPIPGTLVVNIGELLELASNGYLRATVHRVVTPP----AGVERISVPFFFSARLD 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 EHGSEAEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 AL-PEADKLAIEMVKSSQFRGYTRAGGELTK-----GREDWREQLDIGVERQAIAQGPG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 GRIWTQ-YFDRQYTAS-----RAVAREVLRATGTEPDGGVEAFLDCEPLL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 TPAWTRLQGPNQWPAALPDLKPALLAWQSKVTAVAIRLLKAFAQSLDQPEDAF---DPI- 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 RFRYFPQVPEHR-SAEEQPLR------MAPHYDLSMVTLIQQTPCANGFVSLQAEVGG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 AFTDLPYRPDAVLVFCGALATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNAD 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDTTVPTFSLAELQQGLHQ----DEPRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.3%; Score 168; DB 29; Length 366; Best Local Similarity 24.7%; Pred. No. 2.1e-09; Matches 85; Conservative 41; Mismatches 158; Indela 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 ATIPLLGLSEELAAQARGPAS-DPDNPLFRD-VGTNVLKSRLRS 346
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Hinkle, Gregory J.
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CRGANISM: Mesorhizobium loti
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Sequence Seq

ALIGNMENTS

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

374145 segs, 77034267 residues

Searched:

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

	12;	60	120	155	215 233	275	
	Gaps	PTFSL-AELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSE 	AEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWT	QYFDRQYTA-SRAVAREVLRATGTEPDGGVEAFLDC : RLGGPNQWPAALPDLRAAVLRLQAELTAVALALLERIALALGERADFFADLYEGGP	EPLLRFRYFPQVPEHRSAEEQPLRWAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDL :	PYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFELRPNADFTFSV 	
SEC	345; 55;	OLVIDE SRRE	FPSGD	/EAFLD -FFAD	QAEVG	7LRPNA 	
.0679063 PLANTS WITH IMPROVED PHENOTYPES 10/679,063 .5,758	Length 345 Indels 59	ELKSAKU : : : /IDQVE/	GTADNI : GSERPI	repoggy SRAD	ANGFVSI	TESVE	•
Ω		LTDTE	MCYSN EQLD	RATG1 - LALGE	QTPC/ ORDRC	AGSSF	
мркоч	DB 6 09; 134	LTDCG LEGHG	YSDYS : APDWR	AREVI : LERIA	VTLIC	RRDQI PAD	
1.TH I 63	ore 174.5; DB 6; ed. No. 8e-09; Mismatches 134;	KGLFY PGAFY	TNTGS	-SRAV : : VALAL	YDLSM : XDSGL	HVAAP : RVVSP	
9063 NTS W 679,0	Score 174.5; Pred. No. 8e	RCLRD :	STAQI LTR	ROYTA : AELTA	RMAPE : govgpe	KAPRH 	
/1067 D D C PLA C PLA 1-02 415,7	Sc Pr 32;	LATER	GLESE :: 'RVGAE	VLRLC	EEQPI GEGDC	TGGOV	
cation US/10 Michael D TRANSGENIC P 5 (52054)B NUMBER: US/10-02 MBER: 60/415 002-10-02 :: 27373	10.7%; 26.8%; ive	HQDEE ARRDEE	TRRGF1 : IFHGY1	PDLRA	PEHRS! : GRA!	AIATLA : SLLELA	
licati '' Mic 'TRAM -15(5) -15(5) -15(5) -10(5) VMBEI 2002 -2002 -2002 -2002 -2002 -2002 -2002 -2002 -2002 -2002 -2002 -2002 -2002 -2002 -2002	vat	SLOOGI : SEGEA	SPVPTN	PPAALI	YFPQVI : SYP	LVFCG/ - AVNIG	
SULT 1 -10-679-063-16188 Sequence 16188, Application US/10679063 Sequence 16188, Application US/10679063 APPLICANT: Edgerton, Michael D TITLE OF INVENTION: TRANSGENIC FLANTS WIT TILE REFERENCE: 38-15/52054)B CURRENT APPLICATION NUMBER: US/10/679,063 CURRENT FILING DATE: 2003-10-02 PRIOR PLING DATE: 2002-10-02 NUMBER OF FILING DATE: 2002-10-02 NUMBER OF SEQ ID NOS: 27373 SEQ ID NO 16188 LENGTH: 345 TYPE: PRT OKGANISM: Rhodospirillum rubrum -10-679-063-16188	Similarity 11; Conser	FSL-AI LSLKAC	KRAVTS : KRAIDE	OGPNQI	LLRFR) : LLKII	RPDAVI 	277
53-16 16188 WFORM I: Ed INVE ERENC FILLING PLICA PLICA 16180 345 RT M: Rh	ch 1 Sim 81;	6 PT 13 PV	61 AE 72 DE	121 QY : 126 RL	156 EP : 182 DQ	216 PY 234 PP	276 PL 288 PL
SULT 1 -10-679-063-161 Sequence 16188, GENERAL INFORMA APPLICANT: EGG TITLE OF INVEN FILE REFERENCE CURRENT APPLICA CURRENT APPLICA PRIOR APPLICAT PRIOR PILING D RUMBER OF SEG SEQ ID NO 16188 LENGTH: 345 LENGTH: 3	Query Match Best Local Matches 8			A A	ਜੋ ਜੋ	60 60	N N
RESULT 1 US-10-679-063-16188 Sequence 16188, A GENERAL INFORMATI APPLICANT: EGGET TITLE OF INVENTI FILE REFERENCE: CURRENT FILING DATE CURRENT FILING DATE PRIOR PILING DATE TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: ORGANISM: Rhodo	Query Ma Best Lo	상 옵	& 8	දු පු	S G	상 원	상 임
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Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

BB

Length

Query

Result No.

Pending_Patents_AA_New:*

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3: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

Sequence 16188, A Sequence 22244, A Sequence 23175, A Sequence 63175, A Sequence 63454, A Sequence 1321, A Sequence 1321, A Sequence 9242, Ap Sequence 16, Appl Sequence 66945, A Sequence 66943, A Sequence 6611, A Sequence 6617, A Sequence 6617, A Sequence 6617, A Sequence 15920, A

US-10-679-063-16188
US-10-679-063-16144
US-10-679-063-16144
US-10-425-1144-58493
US-10-425-1144-6424
US-10-425-1144-6424
US-10-425-1144-72059
US-10-679-063-9242
US-10-679-063-9242
US-10-679-063-9242
US-10-679-063-9242
US-10-679-063-9242
US-10-739-930-7337
US-10-739-930-6723

174.5 169 150 153 153 153 153 153 153 137.5 137.

RESULT 2 US-10-679-063-16144

US-10-425-114A-61294 US-10-425-114A-66617 US-10-679-063-8477 US-10-679-063-15220 US-10-679-063-9241

131 131 130.5 130.5 128.5 128

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186 YPP---RAAEDADOGVGAHKDYGYLALLLQQDEV---GGLQVQREDGEWIDAVPV-PDAFVFN 240
                                                                                         133 LPELRDIVLRW-----QAEALR-VSREVLRALAAALGODEGYFDQWFDDEAAVHVKIVH 185
        76 LNSP---QFRGYTRTGTEYTAGSAYWREQIDIGPEREALALGPDDPDYLRLIGPNQWPSA 132
                                                   114 -----DFGRIWTQYFDRQYTASRAVAREVLRATGT---EPDGGVEAFLDCEPLLRFRYFP
                                                                                                                                     166 QVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 375;
                                                                                                                                                                                                                                                     241 IGEMLEIATQGYLKATQHRVVSPQ----AGVHRYSIPFFLGPRLD 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49; Mismatches 119; Indels
                                                                                                                                                                                                                            226 CGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Clone ID: LIB3587-225-H12_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.5%; Score 155; DB 6; Best Local Similarity 23.4%; Pred. No. 6.7e-07; Matches 78; Conservative 49; Mismatches 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 PIMPTTDCLIG-PAREFLSDDNPPCYRTLTPADF 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 FLRPNADFTFSVPLARECGFDVSLDGETATFQDW 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-10-425-114A-63175
; Sequence 63175, Application US/10425114A
; GENERAL INFORMATION:
; ARPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPE----- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---NLFPSG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 LPVLDĽSRFRSDTAERAEFLRDVŘĎAAFGPĞFFÝLVGHĞISĎRLIRDVLFASRNFFAL-P 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAEK---RAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 EADKLDIEMINSP---HFRGYTRAGREFTR-----GQPDWREQLDVGAEREAFPLSRSA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----HRSAEEQPLRMAPHYDLSMVTLIQQTPCA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 NGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 VPTFSLAELQQG-LHQDEFRRCLRD----KGLFYLTDCGLTDTELKSAKDLVIDFFEHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LABLOOGLHODEFRRCLRDKGLFYLTDCG----LTDTELKSAKDLVIDFFEHGSEAEKRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 TSSVFFLRPNADFTFSV----PLARECGFDVSLDGETATFQDWIGGNYVNIRRTS 309
                                              APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Edgereron, Michael D
TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REPERENCE: 38-15(52054)B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 22244
                                                                                                                                                                                                                                                                                                                                                         10.3%; Score 169; DB 6; Length 412; 23.9%; Pred. No. 3.4e-08; Live 39; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.8%; Score 160; DB 6; Length 342;
28.1%; Pred. No. 2e-07;
ive 33; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTSPVPTMRRGFTGLESESTAQITNTGSYSDYS----MCYSMGTAD----
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; ORGANISM: Streptomyces hygroscopicus subsp. yingchengensis
US-10-679-063-22244
Sequence 16144, Application US/10679063
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22244, Application US/10679063
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             ORGANISM: Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80; Conservative
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Matches 85; Conserv
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                                                                                                                                                                                                                                                                                                                 US-10-679-063-16144
                                                                                                                                                                                                                            SEQ ID NO 16144
                                                                                                                                                                                                                                                     LENGTH: 412
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Best Local S:
Matches 80
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APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Soreen, Serven E APPLICANT: Serven E APPLICANT: Serven E APPLICANT: Tabaska, Jack B APPLICANT: Cao, Yongwei E APPLICANT: Cao, Yongwei F TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement CURRENT APPLICATION NUMBER: US/10/425,114A CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 58493 LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 PAEDKA------GLYSEDTGRATRIYSSTMFDTGAEKYWRDCLRLACS---FP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 S-GDFGRIW-----TQYFDRQYTASRAVAREVLR----ATGTEPD------GGVEAF 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 BAEKRAVTSPVPTMRRGFTGLESESTAQIT-----NTGSYSDYSMÇYSMGTADNLFP 111
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zoreen, Zoreen, Steven E
APPLICANT: Goreen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION UNDERS: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 53454
LENGTH: 377
                                                                                                                                                                                                                                                                                                                    60 BAEKRAVTSPVPTWRRGFTGLESESTAQIT-----NTGSYSDYSMCYSMGTADNLFP 111
                                                                                                                                                                                                                                                                                    112 S-GDFGRIW------TQYFDRQYTASRAVAREVLR----ATGTEPD------GGVEAF 152
                                                                                                                                                                                                                                                                                                                                                                                         153 LDCEPLLRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAF 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 TDLPYR-----PDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVF 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 LEVAYRGDWIRVEPVPGAFVVNFGCQLEVVTNGILKSIEHRVMTN-----LGVARTTVAT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 EAEKRAVTSPVPTMRRGFTGLESESTAQIT-----NTGSYSDYSMCYSMGTADNLFP 111
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                                                                             4 TVPTFSLAELQQGLHQDEPRRCL----RDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGS
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                             Indels
     23.4%; Pred. No. 1e-06;
tive 48; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 FIMPTIDCLIG-PAMEFLSDDNPPCYRTLTFGDF 345
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US-10-425-114A-53454
                          78; Conservative
Best Local Similarity
Matches 78; Conserv
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Wordleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
FURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                               APPLICANT: Cao, Yongwei Title OF INVENTION: Diants and Uses and Other Molecules Associated With TITLE OF INVENTION: Diants and Uses Thereof for Plant Improvement FILE REPRENCE: 38-21(53313) B CURRENT APPLICATION NUMBER: US/10/425,114A CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 63175 LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 PAEDKA------GLYSEDTGRATRIYSSTMFDTGAEKYWRDCLRLACS---FP 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.4%; Score 154; DB 6; Length 352; Best Local Similarity 23.4%; Pred. No. 7.7e-07; Matches 78; Conservative 49; Mismatches 119; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.3%;
                       Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
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                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Zea mays
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                             APPLICANT:
APPLICANT:
APPLICANT:
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| Sequence 4, Application US/10481381
| Sequence 4, Application US/10481381
| Seguence 4, Application US/10481381
| APPLICANT: Okawa, Miho
| APPLICANT: Matsucka, Makoto
| APPLICANT: Aphlkari, Motoyuki
| TITLE OF INVENTION: 8d1 gene involved in plant semidwarfing and uses thereof
| FILE REFERENCE: SHZ-01808
| FILE REFERENCE: SHZ-01808
| FURRENT APPLICATION NUMBER: US/10/481,381
| CURRENT APPLICATION NUMBER: US/10/481,381
| PRIOR FILING DATE: 2003-12-18
| PRIOR FILING DATE: 2001-06-19
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 4
| LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                         145 FSFKLPWKETLSFRSSAQPDSSNIVQDY-LCNTWG--EDFKP---FGKVVQDYCDAMSTL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 GPFQVSEHGVDAALARAALDGASDFFRLPLAEKRRA--RRVPGTVSGYTSAHADRFASKL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 QITNTGSYSDYSMCYSMGTAD----NLFPSGDF---GRIWTQYFDRQYTASRAVAREVLR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 PWKETLSFGFHDRAAAPVVADYFSSTLGP--DFAPMGRVYOKYCEEMKELSLTIMELLEL 209
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                                                                                                                                                                                                                                                                                      92 GFFLVVNHGVDDKLIAHAHQYIDYFFELPMSAKQRA-----QRKVGEHCGYASSFTGR 144
                                                                                                                                                                                                                                                                                                                                                       80 ------LESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFGRIWTQYFDRQYTA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFF--QVPEHRSAEEQPLRMAPHYDLS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 SLIILHQD-----QVGGLQVFVDEEWRSITPNFNAFVVNIGDTFWALSNGRYKS 301
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                                                                                                                                                       Length 379;
                                                                                                                                                       9.3%; Score 152; DB 6; Length 37
24.3%; Pred. No. 1.3e-06;
tive 40; Mismatches 105; Indels
                                                                                                                                                                                                                                                          30 GLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVTSPVPTMRR--
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24.8%; Pred. No. 2.9e-06;
tive 40; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 CLHRAVVNSK-----TPRKSLAFFLCPKNDKVVSPP 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 IAGSSRTSSVFFLRPNAD 270
                                                                                                                                                                              Best Local Similarity 24.39
Matches 67; Conservative
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Best Local Similarity 24.8'
Matches 64; Conservative
; SEQ ID NO 13321
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Fagus sylvatica
US-10-679-063-13321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Oryza sativa
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US-10-481-381-4
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                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                      APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Serven E
APPLICANT: Screen, Serven E
APPLICANT: Tabaska, Jack E
APPLICANTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 PAEDKA-------GLYSEDTGRATRIYSSTMFDTGGEKYWRDCLRLACS---FP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 AVGDSAAAWPDKPRRLREVVERFTVQTRGLGMBILRLLCEGLGLRPDYLEGDISGG---- 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAEKRAVTSPVPTMRRGFTGLESESTAQIT-----NTGSYSDYSMCYSMGTADNLFP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-GDFGRIW-----TQYFDRQYTASRAVAREVLR----ATGTEPD-----GGVEAF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 IDCEPLIRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQOTPCANGFVSLQAEVGGAF 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 TDLPYR-----PDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVF 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 TVPTFSLAELQQGLHQDEFRRCL----RDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGS
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GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15 (52054)B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
9.3%; Score 153; DB 6; Length 372;
Best Local Similarity 23.4%; Pred. No. 1e-06;
Matches 78; Conservative 48; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Clone ID: LIB3245-358-A7_FLI.pep
US-10-425-114A-72059
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                                                                                                                               314 FIMPTTĎCLIG-PAÁBFLSDĎNPPCYRTLŤRGĎF 346
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                                                                                                                                                                                                                                                       Sequence 72059, Application US/10425114A
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays
                                                                                                                                                                                                           RESULT 8
US-10-425-114A-72059
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Sequence 16, Application US/10257494A GENERAL INFORMATION:
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ORGANISM: Arabidopsis thaliana
                     59 SEAEKRAVTSPVPTMRR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 VYSRPADA--KDVQGYGTKLQKEVEGKKSWVDHL--------FHRVWPPSSI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --OYFDRQYTASRAVAREVLR------ATGTEPDGGV--EAF--LDCEPLLRF 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDA
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GENERAL INFORMATION:
APPLICANT: BASE PLANT SCIENCE GMBH
APPLICANT: BASE PLANT SCIENCE GMBH
TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS IV
FILE REFERENCE: 16313-0236
CURRENT APPLICATION NUMBER: PCT/US03/24364
CURRENT PILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: 02 60/400,803
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PARENTING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PARENTING DATE: 2003-08-04
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PARENTING DATE: 2003-08-04
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                                                                                                                                            APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
TILE REFERENCE: 38-15 (52054)B
CURRENT APPLICATION NUMBER: US/10/679, 063
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415, 758
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 9242
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 335;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.4%; Score 137.5; DB 6; Length 21.8%; Pred. No. 2.8e-05; tive 47; Mismatches 124; Indels
                                                                              RESULT 11
2.10-679-063-9242
Sequence 9242, Application US/10679063
GENERAL INFORMATION:
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 21.8<sup>†</sup>
Matches 63, Conservative
                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Citrus unshiu US-10-679-063-9242
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PCT-US03-24364-36
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APPLICANT: AN, GYN-HEUNG
APPLICANT: ANG, HOUG-GOU
APPLICANT: ANG, KI-HWAN
APPLICANT: DAKK, YONG-JOO
APPLICANT: DAKK, YONG-JOO
APPLICANT: DAKK, YONG-JOO
APPLICANT: DAKK, YONG-JOO
APPLICANT: DEE, SANG-YEB
TITLE OF INVENTION: A PROMOTER CV200xP WHICH REGULATES THE INTEGUMENT-SPECIFIC
TITLE OF INVENTION: SEEDS OF WATERMELON AND A METHOD FOR GENERATING SEEDLESS
TITLE OF INVENTION: FRUITS USING THE PROMOTER
FILE REFERENCE: 7022-0003
TITLE OF INVENTION: FRUITS USING THE PROMOTER
FILE REFERENCE: 2003-08-16
FRIOR PELICATION NUMBER: DCT/KR00/01127
FRIOR APPLICATION NUMBER: PCT/KR00/1127
FRIOR APPLICATION NUMBER: RX 2000/18483
FRIOR FILING DATE: 2000-10-09
FRIOR APPLICATION NUMBER: X 2000/18483
FRIOR FILING DATE: 2000-10-09
SPROR APPLICATION NUMBER: RX 2000/18483
SSOFIL NO 16
SSOFIL NO 16
LENGTH: 380
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GFTG-LESESTAQIINTGSYSDYSMCYSMGTADN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 VPLIDLAGFLSGDSCLASEATRLVSKAATKHGFFLITNHGV-DESLLSRAYLHMDSFFKA 116
                                                                   117 PACEKO-----KAORKWGESSGYASSFVGRFSSKLPWKETLSFKFSPEEKIHSOTVKD-
                                                                                                                                               109 LFPS-----GDFGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRF
                                                                                                                                                                                                                                                                                                   162 RYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 VLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVP 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281 FVVNIGDTFMALTNGRYKSCLHRAVVNSERE-----RKTFAFFLCPKGEKVVKPP 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Solar E
APPLICANT: Solar E
APPLI
Sequence 7737, Application US/10739930
GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
TITLE OF INVENTION:
PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION:
FILE REPERENCE: 38-21 [53377]
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
SEQ ID NO 7737
LENGTH: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285 GG---LEVLVDGEWRPVRPVPGAMVINIGDTFMALSNGRYKSCLHRAVVNQR----RAR 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : | : | : | : | 13 GFFQVCGHGVDAALGRAALDGASDFFRLPLAEKQRA--RRVPGTVSGYTSAHADRFAAKL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGTEPDGGV-EAFLDCEPLLRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 NGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 --QITNTGSYSDYS-----MCYSMGTADNLFPSGDFGRIWTQYFDRQYTASRAVAREVUR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 SLGVELRGYYREFFEDSRSIMRCNYYPPCPE----PERTLGTGPHCDPTALTILLQDXDV 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 GLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVTSPVPTMRRGFTGLESESTA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
8.3%; Score 135.5; DB 6; Length 405;
Best Local Similarity 24.2%; Pred. No. 5.5e-05;
Matches 61; Conservative 41; Mismatches 123; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
; OTHER INFORMATION: Clone ID: ZEAMA-23APR03-C24992_1.p
US-10-739-930-7737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(405)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 TSSVFFLRPNAD 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337 RSLAFFLCPRED 348
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-10-425-114A-66945
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DB 6; Length 385;

Score 133;

8.18;

Query Match

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                                                                                                                                                                                                                                                                                                               233 PDLVWGLSAHSDGSAVTVLQQDV---GCAGLQVRGKGGAWVPVHPVPHALVVNIGDTLEV 289
                                                                                                                                   62 EKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGT-----ADNLFPS--G 113
                                                                                                                                                            177 GFGETLEAYSAEVGELCRILARIAETLGLAPATFADMFGEAVQAVRMNFYPPCPR--- 232
                                                                                                                                                                                                                                                                                      174 EEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAE-VGGAFTDLPYRPDAVLVFCGAIATL 232
                                                                                    114 DFGRIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSA 173
                                                          5 VPTFSLAELQQ----GLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSBA
                       34; Gaps
   1 Similarity 21.9%; Pred. No. 9e-05; 61; Conservative 43; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                              233 VTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNAD 270
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Matches 61; Conserva
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Search completed: February 3, 2004, 17:43:36 Job time : 24 secs